SEQUENCE LISTING

<110> Genentech, Inc.
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<213> Homo sapiens

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Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
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Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
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Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
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Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
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Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
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Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
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Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
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Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
145 150 155 160

Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
180 185 190

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
225 230 235 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
245 250 255

Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
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325 330 335

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340 345 350

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<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

65 70 75 80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
85 90 95

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
100 105 110

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
115 120 125

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
130 135 140

Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
145 150 155 160

Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
165 170 175

Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
180 185 190

Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
195 200 205

Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
210 215 220

Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
225 230 235 240

Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
245 250 255

Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
260 265 270

Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
275 280 285

Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
290 295 300

Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
305 310 315 320

His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
325 330 335

Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 6
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<210> 7
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 7
taagtccggc acattacagg tc 22

<210> 8
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 9
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<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 10
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<210> 11
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<212> DNA
<213> Homo sapiens

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<211> 164
<212> PRT
<213> Homo sapiens

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20 25 30

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
65 70 75 80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
85 90 95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
115 120 125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
130 135 140

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
145 150 155 160

His Asp Pro Gly

<210> 13
<211> 533
<212> DNA
<213> Homo sapiens

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<223> a, t, c or g

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<222> (80)
<223> a, t, c or g

<220>
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<223> a, t, c or g

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<223> a, t, c or g

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<223> a, t, c or g

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<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 14

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<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 15
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<210> 16
<211> 50
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<210> 17
<211> 960
<212> DNA
<213> Homo sapiens

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<210> 18
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<213> Homo sapiens

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Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
180 185

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 19
tgctgtgcta ctcctgcaaa gccc 24

<210> 20
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 20
tgcacaagtc ggtgtcacag cacg 24

<210> 21
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 21
agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg 44

<210> 22
<211> 1200
<212> DNA
<213> Homo sapiens

<400> 22
cccacgcgtc cgaacctctc cagcgatggg agccgcccgc ctgctgccca acctcactct 60
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gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180
caagcacgtg caggtcaccg ggcgtcgcat ctccgccacc gccgaggacg gcaacaagtt 240
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cgcccggcac gagggctggt tcatggcctt cacgcggcag gggcggcccc gccaggcttc 480
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<210> 23
<211> 205
<212> PRT
<213> Homo sapiens

<400> 23

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Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu
  1               5                  10                  15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met
             20                  25                  30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
         35                  40                  45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
     50                  55                  60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
 65                  70                  75                  80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
                 85                  90                  95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
            100                 105                 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
        115                 120                 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
    130                 135                 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
145                 150                 155                 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
                165                 170                 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
            180                 185                 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
        195                 200                 205
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<210> 24
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 24
cagtacgtga gggaccaggg cgccatga 28

<210> 25

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 25
ccggtgacct gcacgtgctt gcca 24

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<220>
<221> modified_base
<222> (21)
<223> a, t, c or g

<400> 26
gcggatctgc cgcctgctca nctggtcggt catggcgccc t 41

<210> 27
<211> 2479
<212> DNA
<213> Homo sapiens

<400> 27
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ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180
tccagtcatt ttgattttgc tgtttatttt ttttttcttt ttctttttcc caccacattg 240
tattttattt ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300
ctttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360
tcctggcctg ccctagtgtg tgccgctgcg acaggaactt tgtctactgt aatgagcgaa 420
gcttgacctc agtgcctctt gggatcccgg agggcgtaac cgtactctac ctccacaaca 480
accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtcg gtgcacacgg 540
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tgaagcttga agagctgcac ctggatgaca actccatatc cacagtgggg gtggaagacg 720
gggccttccg ggaggctatt agcctcaaat tgttgttttt gtctaagaat cacctgagca 780
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caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

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aaggggtttt tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200
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acgtgcgggg tttcatgtgc caaggtcctg aacaagtccg ggggatggcc gtcagggaat 1320
taaatatgaa tcttttgtcc tgtcccacca cgacccccgg cctgcctctc ttcaccccag 1380
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gaagctacac gcctccaact cctaccacat cgaaacttcc cacgattcct gactgggatg 1500
gcagagaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560
atgatacttc cattcaagtc agctggctct ctctcttcac cgtgatggca tacaaactca 1620
catgggtgaa aatgggccac agtttagtag ggggcatcgt tcaggagcgc atagtcagcg 1680
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ccacccatgc ctcctatctg aacaacggca gcaacacagc gtccagccat gagcagacga 1860
cgtcccacag catgggctcc ccctttctgc tggcgggctt gatcgggggc gcggtgatat 1920
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cctcccagaa gtggaaatac aaccggggcc ggcggaaaga tgattattgc gaggcaggca 2040
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tctttgcttt ttaaatctt                                            2479

<210> 28
<211> 660
<212> PRT
<213> Homo sapiens

<400> 28
Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
  1               5                  10                  15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
             20                  25                  30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
         35                  40                  45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
     50                  55                  60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
 65                  70                  75                  80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
                 85                  90                  95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
            100                 105                 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
        115                 120                 125
```

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Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
    130                 135                 140

Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
145                 150                 155                 160

Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
                165                 170                 175

Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
            180                 185                 190

Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
        195                 200                 205

Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
    210                 215                 220

Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
225                 230                 235                 240

Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
                245                 250                 255

Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
            260                 265                 270

Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
        275                 280                 285

Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
    290                 295                 300

Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
305                 310                 315                 320

Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
                325                 330                 335

Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
            340                 345                 350

Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro
        355                 360                 365

Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
    370                 375                 380

Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
385                 390                 395                 400

Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg
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                405                 410                 415

Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val
            420                 425                 430

Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met
        435                 440                 445

Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly
    450                 455                 460

Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu
465                 470                 475                 480

Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu
                485                 490                 495

Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala
            500                 505                 510

Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser
        515                 520                 525

His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala
    530                 535                 540

Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser
545                 550                 555                 560

Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys
                565                 570                 575

Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly
            580                 585                 590

Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln
        595                 600                 605

Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu
    610                 615                 620

Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His
625                 630                 635                 640

Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu
                645                 650                 655

His Cys His Thr
            660
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<210> 29
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 29
cggtctacct gtatggcaac c 21

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 30
gcaggacaac cagataaacc ac 22

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 31
acgcagattt gagaaggctg tc 22

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 32
ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac 46

<210> 33
<211> 3449
<212> DNA
<213> Homo sapiens

<400> 33
acttggagca agcggcggcg gcggagacag aggcagaggc agaagctggg gctccgtcct 60
cgcctcccac gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

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ttatacaata ttaaaattca ccacttcag 3449

<210> 34
<211> 915
<212> PRT
<213> Homo sapiens

<400> 34

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Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
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Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
             20                  25                  30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
         35                  40                  45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
     50                  55                  60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
 65                  70                  75                  80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
                 85                  90                  95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
            100                 105                 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
        115                 120                 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
    130                 135                 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
145                 150                 155                 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
                165                 170                 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
            180                 185                 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
        195                 200                 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
    210                 215                 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His
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225 230 235 240

Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile
245 250 255

Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser
260 265 270

Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His
275 280 285

Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln
290 295 300

Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala
305 310 315 320

Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val
325 330 335

Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu
340 345 350

Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn
355 360 365

Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr
370 375 380

Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys
385 390 395 400

Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu
405 410 415

Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe
420 425 430

Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu
435 440 445

Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser
450 455 460

Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys
465 470 475 480

Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu
485 490 495

His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu
500 505 510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
515 520 525

Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
530 535 540

Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
545 550 555 560

Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
565 570 575

Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
580 585 590

Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
595 600 605

Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
610 615 620

Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
625 630 635 640

Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu
645 650 655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
660 665 670

Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
675 680 685

Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
690 695 700

Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
705 710 715 720

Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
725 730 735

Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
740 745 750

Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
755 760 765

Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
770 775 780

Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
900 905 910

Arg Tyr Arg
915

<210> 35
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 35
gtgaccctgg ttgtgaatac tcc 23

<210> 36
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 36
acagccatgg tctatagctt gg 22

<210> 37
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37
gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag 45

<210> 38
<211> 1813
<212> DNA
<213> Homo sapiens

<400> 38
ggagccgccc tgggtgtcag cggctcggct cccgcgcacg ctccggccgt cgcgcagcct 60
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tttgtatgaa aaa 1813

<210> 39
<211> 390
<212> PRT
<213> Homo sapiens

<400> 39
Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

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Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln
            20                  25                  30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val
        35                  40                  45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
    50                  55                  60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
65                  70                  75                  80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro
                85                  90                  95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg
            100                 105                 110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val
        115                 120                 125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
    130                 135                 140

Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu
145                 150                 155                 160

Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
                165                 170                 175

Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
            180                 185                 190

Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
        195                 200                 205

Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys
    210                 215                 220

Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
225                 230                 235                 240

Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
                245                 250                 255

Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His
            260                 265                 270

Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
        275                 280                 285
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Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
370 375 380

Gln Ala Gly Ser Leu Val
385 390

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 40
agggtctcca ggagaaagac tc 22

<210> 41
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 41
attgtgggcc ttgcagacat agac 24

<210> 42
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 42
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 43
gtgtgacaca gcgtgggc 18

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 44
gaccggcagg cttctgcg 18

<210> 45
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 45
cagcagcttc agccaccagg agtgg 25

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 46
ctgagccgtg ggctgcagtc tcgc 24

<210> 47

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 47
ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48
<211> 2822
<212> DNA
<213> Homo sapiens

<400> 48
cgccaccact gcggccaccg ccaatgaaac gcctcccgct cctagtggtt ttttccactt 60
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gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatggtg 180
tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240
ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300
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caaactgcca tttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420
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acctccacaa attgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2820
aa 2822

<210> 49
<211> 690
<212> PRT
<213> Homo sapiens

<400> 49
Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
1 5 10 15

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
20 25 30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
35 40 45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
65 70 75 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
85 90 95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
100 105 110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
115 120 125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
130 135 140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
145 150 155 160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
165 170 175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

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        180                 185                 190

Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val
        195                 200                 205

Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys
    210                 215                 220

Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe
225                 230                 235                 240

Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys
                245                 250                 255

Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met
            260                 265                 270

Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala
        275                 280                 285

Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser
    290                 295                 300

Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln
305                 310                 315                 320

Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile
                325                 330                 335

Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys
            340                 345                 350

Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser
        355                 360                 365

Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp
    370                 375                 380

Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser
385                 390                 395                 400

Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly
                405                 410                 415

Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln
            420                 425                 430

Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr
        435                 440                 445

Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys
    450                 455                 460
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Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
675 680 685

Leu Arg
690

<210> 50
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (61)

<223> a, t, c or g

<400> 50
tggaaacata tcctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaatggca atgttgcagt tgcattttta tattataaga 120
gtattggtcc ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccacccacat tatatgaact tgaaaaaata acatttacat taagtcatcg aaaggtcaca 300
gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
tggtcttcag agggctgtga gctgacatac tcaaatgaga cccacacctc atgccgctgt 420
aatcacctga cacattttgc aattttgatg tcctctggtc cttccattgg tattaaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 51
ggtaatgagc tccattacag 20

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 52
ggagtagaaa gcgcatgg 18

<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 53
cacctgatac catgaatggc ag 22

<210> 54
<211> 18
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 54
cgagctcgaa ttaattcg 18

<210> 55
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 55
ggatctcctg agctcagg 18

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 56
cctagttgag tgatccttgt aag 23

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 57
atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt 50

<210> 58
<211> 2137
<212> DNA
<213> Homo sapiens

<400> 58
gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60
cgctaagcga ggcctcctcc tcccgcagat ccgaacggcc tgggcggggt caccccggct 120

gggacaagaa gccgccgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180
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cccaggcccc ccaccttatg tcaacctgca cttcttgttc aaaaatcagg aaaagaaaag 1920
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gaaccctttc cccagcactt ggttttccaa catgatattt atgagtaatt tattttgata 2040
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<210> 59
<211> 216
<212> PRT
<213> Homo sapiens

<400> 59
Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
1 5 10 15

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
210 215

<210> 60
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 60
atccgcccag atggctacaa tgtgta 26

<210> 61
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 61
gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta 42

<210> 62
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 62
ccagtccggt gacaagccca aa 22

<210> 63
<211> 1295
<212> DNA
<213> Homo sapiens

<400> 63
cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60
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gctgctgctg cgctacctgg tggtcgccct gggctatcat aaggcctatg ggttttctgc 180
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<210> 64
<211> 312
<212> PRT
<213> Homo sapiens

<400> 64
Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr
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Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
20 25 30

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Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
        35                  40                  45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
    50                  55                  60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
65                  70                  75                  80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
                85                  90                  95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
            100                 105                 110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
        115                 120                 125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
    130                 135                 140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
145                 150                 155                 160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
                165                 170                 175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
            180                 185                 190

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
        195                 200                 205

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
    210                 215                 220

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
225                 230                 235                 240

Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
                245                 250                 255

Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
            260                 265                 270

Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
        275                 280                 285

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
    290                 295                 300

Gly Gly Ser Arg Gly Gln Glu Phe
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305 310

<210> 65
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 65
atcgttgtga agttagtgcc cc 22

<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 66
acctgcgata tccaacagaa ttg 23

<210> 67
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 67
ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

<210> 68
<211> 2639
<212> DNA
<213> Homo sapiens

<400> 68
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gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180
aaataaatga attactcaat ctcctatgac catctataca tactccacct tcaaaaagta 240
catcaatatt atatcattaa ggaaatagta accttctctt ctccaatatg catgacattt 300
ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtggttcta 360
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actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480
tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtac 540

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taaatctctg ggaagcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580
taggtttacc aacaaatatg tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

<210> 69
<211> 708
<212> PRT
<213> Homo sapiens

<400> 69
Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
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Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
50 55 60

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Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn
 65                  70                  75                  80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
                85                  90                  95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
            100                 105                 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
        115                 120                 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
    130                 135                 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
145                 150                 155                 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
                165                 170                 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
            180                 185                 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
        195                 200                 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
    210                 215                 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
225                 230                 235                 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
                245                 250                 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
            260                 265                 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
        275                 280                 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
    290                 295                 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
305                 310                 315                 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
                325                 330                 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly
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340 345 350

Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn
355 360 365

Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr
370 375 380

Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro
385 390 395 400

Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met
405 410 415

Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu
420 425 430

Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala
435 440 445

Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu
450 455 460

Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr
465 470 475 480

Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys
485 490 495

Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys
500 505 510

Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys
515 520 525

Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser
530 535 540

Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr
545 550 555 560

Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys
565 570 575

Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys
580 585 590

Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn
595 600 605

Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn
610 615 620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
690 695 700

Thr Asn Met Ser
705

<210> 70
<211> 1305
<212> DNA
<213> Homo sapiens

<400> 70
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ttaccacgct tgttggagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180
gaatctggta gacctgtggt taacccgttc cctctccatg tgtctcctcc tacaaagttt 240
tgttcttatg atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300
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tcttcctcct gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420
tgaaattttt aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgtc 540
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600
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caccccttaa ttgtaccccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200
tagatccatc tcactattta ataatgaaat ttatttttt aatttaaaag caaataaaag 1260
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<210> 71
<211> 259
<212> PRT
<213> Homo sapiens

<400> 71

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Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu
 1               5                  10                  15

Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser
            20                  25                  30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
        35                  40                  45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
    50                  55                  60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
65                  70                  75                  80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
                85                  90                  95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
            100                 105                 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
        115                 120                 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
    130                 135                 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
145                 150                 155                 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
                165                 170                 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
            180                 185                 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
        195                 200                 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
    210                 215                 220

Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
225                 230                 235                 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser
                245                 250                 255

Thr Val Val
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<210> 72
<211> 2290

<212> DNA
<213> Homo sapiens

<400> 72
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ggaccccacc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
aaaaaaaaaa 2290

<210> 73
<211> 620
<212> PRT
<213> Homo sapiens

<400> 73
Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
1 5 10 15

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Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
            20                  25                  30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
        35                  40                  45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
    50                  55                  60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
65                  70                  75                  80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
                85                  90                  95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
            100                 105                 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
        115                 120                 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
    130                 135                 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
145                 150                 155                 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
                165                 170                 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
            180                 185                 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
        195                 200                 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
    210                 215                 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
225                 230                 235                 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
                245                 250                 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
            260                 265                 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
        275                 280                 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
    290                 295                 300
```

```
Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
305                 310                 315                 320

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
                325                 330                 335

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
            340                 345                 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
        355                 360                 365

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
    370                 375                 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
385                 390                 395                 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
                405                 410                 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
            420                 425                 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
        435                 440                 445

Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
    450                 455                 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
465                 470                 475                 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
                485                 490                 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
            500                 505                 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
        515                 520                 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
    530                 535                 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
545                 550                 555                 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
                565                 570                 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn
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580 585 590

Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser
595 600 605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile
610 615 620

<210> 74
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 74
tcacctggag cctttattgg cc 22

<210> 75
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 75
ataccagcta taaccaggct gcg 23

<210> 76
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 76
caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg gg 50 52

<210> 77
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 77
ccatgtgtct cctcctacaa ag 22

<210> 78
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 78
gggaatagat gtgatctgat tgg 23

<210> 79
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 79
cacctgtagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg 50

<210> 80
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 80
agcaaccgcc tgaagctcat cc 22

<210> 81
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 81
aaggcgcggt gaaagatgta gacg 24

<210> 82

<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 82
gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 83
cccacgcgtc cgcacctcgg ccccgggctc cgaagcggct cgggggcgcc ctttcggtca 60
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aaaca 1685

<210> 84
<211> 398
<212> PRT
<213> Homo sapiens

<400> 84

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Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Leu Phe Ala
 1               5                  10                  15

Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
            20                  25                  30

Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
        35                  40                  45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
    50                  55                  60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
65                  70                  75                  80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
                85                  90                  95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
            100                 105                 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
        115                 120                 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
    130                 135                 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
145                 150                 155                 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
                165                 170                 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
            180                 185                 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
        195                 200                 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
    210                 215                 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
225                 230                 235                 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
                245                 250                 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
            260                 265                 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
        275                 280                 285
```

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
385 390 395

<210> 85
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 85
gctaggaatt ccacagaagc cc 22

<210> 86
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 86
aacctggaat gtcaccgagc tg 22

<210> 87
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 87
cctagcacag tgacgaggga cttggc 26

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 88
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 89
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90
<211> 2755
<212> DNA
<213> Homo sapiens

<400> 90
gggggttagg gaggaaggaa tccaccccca ccccccccaaa ccctttttctt ctcctttcct 60
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gctgttactt tgtgatgaga tcggggatga attgctcgct ttaaaaatgc tgctttggat 180
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<210> 91
<211> 696
<212> PRT
<213> Homo sapiens

<400> 91

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Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
  1               5                  10                  15

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
             20                  25                  30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
         35                  40                  45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
     50                  55                  60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
 65                  70                  75                  80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
                 85                  90                  95
```

```
Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
            100                 105                 110

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
        115                 120                 125

Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
    130                 135                 140

Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
145                 150                 155                 160

Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
                165                 170                 175

Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
            180                 185                 190

Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
        195                 200                 205

Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
    210                 215                 220

Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
225                 230                 235                 240

Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
                245                 250                 255

Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
            260                 265                 270

Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
        275                 280                 285

Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
    290                 295                 300

Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg
305                 310                 315                 320

Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala
                325                 330                 335

Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly
            340                 345                 350

Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
        355                 360                 365

Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
    370                 375                 380
```

```
Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
385                 390                 395                 400

Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn
                405                 410                 415

Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser
            420                 425                 430

Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn
        435                 440                 445

Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro
    450                 455                 460

Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn
465                 470                 475                 480

Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu
                485                 490                 495

Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala
            500                 505                 510

Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly
        515                 520                 525

Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala
    530                 535                 540

Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr
545                 550                 555                 560

Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu
                565                 570                 575

Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His
            580                 585                 590

Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser
        595                 600                 605

Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu
    610                 615                 620

Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val
625                 630                 635                 640

Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser
                645                 650                 655

Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr
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660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp
675 680 685

Cys Gly Ser His Ser Leu Ser Asp
690 695

<210> 92
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 92
gttggatctg ggcaacaata ac 22

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 93
attgttgtgc aggctgagtt taag 24

<210> 94
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 94
ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95
<211> 2226
<212> DNA
<213> Homo sapiens

<400> 95
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gctgcaccgg gcctggcagc gctccgcaca catttcctgt cgcggcctaa gggaaactgt 120
tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg 180

gaggggaagg gaggggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
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ccagctgcac agcgccgctc tggacttcag tccacctggg accgaggtga gtgcgctctg 960
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tgggggggacc ggggtgccca ccaggcgccc gccggccact gcaaccagcc ccgtgccgca 1260
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gttgat 2226

<210> 96
<211> 490
<212> PRT
<213> Homo sapiens

<400> 96
Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
1 5 10 15

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
50 55 60

```
Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
 65                  70                  75                  80

Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
                 85                  90                  95

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
            100                 105                 110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
        115                 120                 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
    130                 135                 140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
145                 150                 155                 160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
                165                 170                 175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
            180                 185                 190

Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
        195                 200                 205

Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
    210                 215                 220

Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
225                 230                 235                 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
                245                 250                 255

Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
            260                 265                 270

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
        275                 280                 285

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
    290                 295                 300

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
305                 310                 315                 320

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
                325                 330                 335

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln
```

```
            340                 345                 350

Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala
        355                 360                 365

Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr
    370                 375                 380

Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe
385                 390                 395                 400

Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr
                405                 410                 415

Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln
            420                 425                 430

Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu
        435                 440                 445

Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val
    450                 455                 460

Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu
465                 470                 475                 480

Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala
                485                 490
```

<210> 97
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 97
tggaaggaga tgcgatgcca cctg 24

<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 98
tgaccagtgg ggaaggacag 20

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 99
acagagcaga gggtgccttg 20

<210> 100
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 100
tcagggacaa gtggtgtctc tccc 24

<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 101
tcagggaagg agtgtgcagt tctg 24

<210> 102
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 102
acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct 50

<210> 103
<211> 2026
<212> DNA
<213> Homo sapiens

<400> 103
cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgccct gccggccgcg 120
tatcccccgg ctacctgggc cgccccgcgg cggtgcgcgc gtgagaggga gcgcgcgggc 180
agccgagcgc cggtgtgagc cagcgctgct gccagtgtga gcggcggtgt gagcgcggtg 240
ggtgcggagg ggcgtgtgtg ccggcgcgcg cgccgtgggg tgcaaacccc gagcgtctac 300
gctgccatga ggggcgcgaa cgcctgggcg ccactctgcc tgctgctggc tgccgccacc 360
cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420
ggagagtctg gatttattgg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
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caaaagtgta gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtatta 1260
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ctaaaagtgt caagcgttga cagcttggaa gcgtttattt atacatctct gtaaaaggat 1860
attttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920
gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatatttttа aaggaaaaaa aaaaaa 2026

<210> 104
<211> 415
<212> PRT
<213> Homo sapiens

<400> 104
Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
1 5 10 15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
50 55 60

```
Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
 65                 70                  75                  80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
                85                  90                  95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
            100                 105                 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
        115                 120                 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
    130                 135                 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
145                 150                 155                 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
                165                 170                 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
            180                 185                 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
        195                 200                 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
    210                 215                 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
225                 230                 235                 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
                245                 250                 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
            260                 265                 270

Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
        275                 280                 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
    290                 295                 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
305                 310                 315                 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
                325                 330                 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala
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340 345 350

Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro
355 360 365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu
370 375 380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys
385 390 395 400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys
405 410 415

<210> 105
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 105
ccgattcata gacctcgaga gt 22

<210> 106
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 106
gtcaaggagt cctccacaat ac 22

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 107
gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt 45

<210> 108
<211> 1838
<212> DNA

<213> Homo sapiens

<400> 108
cggacgcgtg ggcggacgcg tgggcggccc acggcgcccg cgggctgggg cggtcgcttc 60
ttccttctcc gtggcctacg agggtcccca gcctgggtaa agatggcccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180
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aactttggag gtggaaacac tgcctgggag gaagagaatt tgtccaaata caaagacagt 360
gagacccgcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420
cgcctgctgg agctgagtga ggagctggtg gagagctggt ggtttcacaa gcagcaggag 480
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cagcagatgt tctttggcat catcatctgt gcactggcca cgctggctgc taagggcgac 1260
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acaggggtgg ggccatcaca gctccctcct gccagctgca tgctgccagt tcctgttctg 1740
tgttcaccac atccccacac cccattgcca cttatttatt catctcagga aataaagaaa 1800
ggtcttggaa agttaaaaaa aaaaaaaaaa aaaaaaaa 1838

<210> 109
<211> 420
<212> PRT
<213> Homo sapiens

<400> 109
Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
 1   5   10   15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
            20   25   30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
        35   40   45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
    50   55   60

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
130 135 140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys
180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
405 410 415

Ile Lys Gly Arg
420

<210> 110
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 110
cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 111
attctgcgtg aacactgagg gc 22

<210> 112
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 112
atctgcttgt agccctcggc ac 22

<210> 113

<211> 1616
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1461)
<223> a, t, c or g

<400> 113
tgagaccctc ctgcagcctt ctcaagggac agccccactc tgcctcttgc tcctccaggg 60
cagcaccatg cagcccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120
cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180
agaggtgccc accctggaca gggccgacat ggaggagctg gtcatcccca cccacgtgag 240
ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300
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gcggctcttc caggagccgg tccccaaggc cgcgctgcac aggcacgggc ggctgtcccc 480
gcgcagcgcc cgggcccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540
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aaagtcctcc accaccactc tggacctaag acctggggtt aagtgtgggt tgtgcatccc 1560
caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114
<211> 366
<212> PRT
<213> Homo sapiens

<400> 114
Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
1 5 10 15

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
20 25 30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
180 185 190

Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
355 360 365

<210> 115
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 115
aggactgcca taacttgcct g 21

<210> 116
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 116
ataggagttg aagcagcgct gc 22

<210> 117
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 117
tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118
<211> 1857
<212> DNA
<213> Homo sapiens

<400> 118
gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc gatggggaca 60
aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120
ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaag 240
tttgaccaag gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaactggt atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctcctctgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540
tacacctggt tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac ccgtgccttc 600
agcaactctt cctatgtcct gaatcccaca acaggagagc tggtctttga tcccctgtca 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaatgctg tgcgcatgga agctgtggag cggaatgtgg gggtcatcgt ggcagccgtc 780
cttgtaaccc tgattctcct gggaatcttg gtttttggca tctggtttgc ctatagccga 840
ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
agtgcccgaa gtgaaggaga attcaaacag acctcgtcat tcctggtgtg agcctggtcg 960
gctcaccgcc tatcatctgc atttgcctta ctcaggtgct accggactct ggcccctgat 1020
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tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140
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tggcgggggt cgcaggaatc tgcactcaac tgcccacctg gctggcaggg atctttgaat 1320
aggtatcttg agcttggttc tgggctcttt ccttgtgtac tgacgaccag ggccagctgt 1380
tctagagcgg gaattagagg ctagagcggc tgaaatggtt gtttggtgat gacactgggg 1440
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ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
agctcttgtt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggatttaaa 1620
accgctgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tggtgcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

<210> 119
<211> 299
<212> PRT
<213> Homo sapiens

<400> 119
Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
290 295

<210> 120
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 120
tcgcggagct gtgttctgtt tccc 24

<210> 121
<211> 50

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 121
tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 122
acacctggtt caaagatggg 20

<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 123
taggaagagt tgctgaaggc acgg 24

<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 124
ttgccttact caggtgctac 20

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 125
actcagcagt ggtaggaaag 20

<210> 126
<211> 1210
<212> DNA
<213> Homo sapiens

<400> 126
cagcgcgtgg ccggcgccgc tgtggggaca gcatgagcgg cggttggatg gcgcaggttg 60
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctcggactag 120
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300
ggattgagcc atgtacccag aaagggcaat gcccaccgcc ccctggcctc ccctgccct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggcgctgcga cggccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagtg 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtccct 660
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagccca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgccacc ctcctccttt 780
tgtcctggct ccgagcccag gagcgcctcc gcccactggg gttactggtg gccatgaagg 840
agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900
ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960
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tcctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080
agctaggatg gggaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200
aagttgcttc 1210

<210> 127
<211> 282
<212> PRT
<213> Homo sapiens

<400> 127
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
85 90 95

Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala
225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln
245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
275 280

<210> 128
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 128
aagttccagt gccgcaccag tggc 24

<210> 129

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 129
ttggttccac agccgagctc gtcg 24

<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 130
gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1837)
<223> a, t, c or g

<400> 131
cccacgcgtc cggtctcgct cgctcgcgca gcggcggcag cagaggtcgc gcacagatgc 60
gggttagact ggcgggggga ggaggcggag gagggaagga agctgcatgc atgagaccca 120
cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaacccga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcggccct gcacagctca 300
cgggcgggtt cgatgacctt caagtgtgtg ctgaccccgg cattcccgag aatggcttca 360
ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaatc atcacttgtc 600
atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatta tgtcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
atcgctgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
ctccaatggt gagtcacgga gatttcgtct gccacccgcg gccttgtgag cgctacaacc 960
acggaactgt ggtggagttt tactgcgatc ctggctacag cctcaccagc gactacaagt 1020
acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatcag 1080
agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaagatt gtggcgttca 1140

cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260
ttgtggtggt agacggcgtg cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320
gcttgagtgc cttaggcccc gggtacatgg cctctgtggg ccagggctgc cccttacccg 1380
tggacgacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440
agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500
ctcccaggtg ccaagagagc acccaccctg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcatccatca tgcccactgg gtgttgttcc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtgagggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132
<211> 490
<212> PRT
<213> Homo sapiens

<400> 132
Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
1 5 10 15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

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                180                 185                 190

Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr
        195                 200                 205

Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys
    210                 215                 220

Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu
225                 230                 235                 240

Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe
                245                 250                 255

Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val
            260                 265                 270

Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr
        275                 280                 285

Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys
    290                 295                 300

Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr
305                 310                 315                 320

Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu
                325                 330                 335

Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His
            340                 345                 350

Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe
        355                 360                 365

Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala
    370                 375                 380

Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val
385                 390                 395                 400

Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr
                405                 410                 415

Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys
            420                 425                 430

Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro
        435                 440                 445

Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile
    450                 455                 460
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Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
485 490

<210> 133
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 133
atctcctatc gctgctttcc cgg 23

<210> 134
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 134
agccaggatc gcagtaaaac tcc 23

<210> 135
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 135
atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct 50

<210> 136
<211> 1815
<212> DNA
<213> Homo sapiens

<400> 136
cccacgcgtc cgctccgcgc cctccccccc gcctcccgtg cggtccgtcg gtggcctaga 60
gatgctgctg ccgcggttgc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120
ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180
tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgcctgc 240
tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

ggccttgtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600
gcgaggtctg cgtggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattcccctt ctcctcctcc 900
ttgtggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960
cagaccctag cacaaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020
cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080
ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200
tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaatgg 1260
ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320
aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380
ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
tccccacgac ctcctgttgg acccccacgt tttggctgta tcctttatcc cagccagtca 1500
tccagctcga ccttatgaga aggtaccttg cccaggtctg gcacatagta gagtctcaat 1560
aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggcaat tctcatatct gttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaa 1815

<210> 137
<211> 382
<212> PRT
<213> Homo sapiens

<400> 137
Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
100 105 110

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Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
        115                 120                 125

Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
    130                 135                 140

Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
145                 150                 155                 160

Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
                165                 170                 175

Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
            180                 185                 190

Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
        195                 200                 205

Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
    210                 215                 220

Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
225                 230                 235                 240

Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
                245                 250                 255

Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
            260                 265                 270

Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
        275                 280                 285

Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
    290                 295                 300

Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
305                 310                 315                 320

Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
                325                 330                 335

Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
            340                 345                 350

Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
        355                 360                 365

Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
    370                 375                 380
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<210> 138

<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 138
gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 139
aagccaaaga agcctgcagg aggg 24

<210> 140
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 140
cagtccaagc ataaaggtcc tggc 24

<210> 141
<211> 1514
<212> DNA
<213> Homo sapiens

<400> 141
ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120
ttgtgtttgc ctcctgcagc ctcaacccgg agggcagcga gggcctacca ccatgatcac 180
tggtgtgttc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgtactg 240
cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300
cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcgtg tttcgacacg gggctcggag 360
tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420
cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
gctgaccaag gtgggcatgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600
tgtggaagac attccctttc tttcaccaac cttcaaccca caggaggtct ttattcgttc 660
cactaacatt tttcggaatc tggagtccac ccgttgtttg ctggctgggc ttttccagtg 720

```
tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
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caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200
gaccctgggg atttttgacc acaaatggcc accgtttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtggtt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg                                                   1514
```

<210> 142
<211> 428
<212> PRT
<213> Homo sapiens

<400> 142

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Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1               5                  10                  15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
             20                  25                  30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
         35                  40                  45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
     50                  55                  60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
 65                  70                  75                  80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
                 85                  90                  95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
            100                 105                 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
        115                 120                 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
    130                 135                 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
145                 150                 155                 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
                165                 170                 175
```

```
Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
            180                 185                 190

Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
        195                 200                 205

Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
    210                 215                 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
225                 230                 235                 240

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
                245                 250                 255

Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
            260                 265                 270

Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
        275                 280                 285

Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
    290                 295                 300

Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
305                 310                 315                 320

Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
                325                 330                 335

Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
            340                 345                 350

Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
        355                 360                 365

Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
    370                 375                 380

Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
385                 390                 395                 400

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
                405                 410                 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
            420                 425
```

<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143
ccaactacca aagctgctgg agcc 24

<210> 144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 144
gcagctctat taccacggga agga 24

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145
tccttcccgt ggtaatagag ctgc 24

<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146
ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg 45

<210> 147
<211> 1686
<212> DNA
<213> Homo sapiens

<400> 147
ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60
cttaaatttc agctcatcac cttcacctgc cttggtcatg gctctgctat tctccttgat 120
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
agctgccagc ggaaccccta gtggtatttt gtatgagcca ccagcagaaa aagagcaaaa 360
ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaacccaga 480
gagctctttc tccccagtcc cagagggtgt caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccgggcc gcaaaggtgg tgtgccggca gctgggatgt gggagggctg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
ctcaggacga gaagcaaccc ttcaggattg cccttctggg ccttgggggа agaacacctg 780
caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
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cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccatttgtcc 1500
tgtttctctg aagaactctg acaaaataca gattttggta ctgaaagaga ttctagagga 1560
acggaatttt aaggataaat tttctgaatt ggttatgggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctggtaactt tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

<210> 148
<211> 347
<212> PRT
<213> Homo sapiens

<400> 148
Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
100 105 110

```
Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
        115                 120                 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
    130                 135                 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
145                 150                 155                 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
                165                 170                 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
            180                 185                 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
        195                 200                 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
    210                 215                 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
225                 230                 235                 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
                245                 250                 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
            260                 265                 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
        275                 280                 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
    290                 295                 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
305                 310                 315                 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
                325                 330                 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val
            340                 345
```

<210> 149
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 149
ttcagctcat caccttcacc tgcc 24

<210> 150
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 150
ggctcataca aaataccact aggg 24

<210> 151
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 151
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt 50

<210> 152
<211> 1427
<212> DNA
<213> Homo sapiens

<400> 152
actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60
acccacgcgt ccgcggacgc gtgggcggac gcgtgggccg gctaccagga agagtctgcc 120
gaaggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180
cctgggcgtc ttcggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240
gaatgctgtg gtggtgatca caggcgccac ctcagggctg ggcaaagaat gtgcaaaagt 300
cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360
gctcatcaga gaacttaccg cttctcatgc caccaaggtg cagacacaca agccttactt 420
ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480
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ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttggccgcc atggcccaac ttgtttattg cagcttataa tggttac 1427

<210> 153
<211> 310
<212> PRT
<213> Homo sapiens

<400> 153
Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210 215 220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
225 230 235 240

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val
260 265 270

Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu
275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu
290 295 300

Arg Lys Ser Lys Asn Ser
305 310

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 154
ggtgctaaac tggtgctctg tggc 24

<210> 155
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 155
cagggcaaga tgagcattcc 20

<210> 156
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 156
tcatactgtt ccatctcggc acgc 24

<210> 157
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 157
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158
<211> 1771
<212> DNA
<213> Homo sapiens

<400> 158
cccacgcgtc cgctggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60
aaaaaaaaaa acacaccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120
cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaaggt 360
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aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720
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aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtgt 960
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tttctgttct acataaaatc agaaacttca agctctctaa ataaaatgaa ggactatatc 1440
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gctagaggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620
agagaatgta cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1771

<210> 159

<211> 300
<212> PRT
<213> Homo sapiens

<400> 159

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Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Pro Leu Leu Ile Val
  1               5                  10                  15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
             20                  25                  30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
         35                  40                  45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
     50                  55                  60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
 65                  70                  75                  80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
                 85                  90                  95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
            100                 105                 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp
        115                 120                 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
    130                 135                 140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
145                 150                 155                 160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
                165                 170                 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
            180                 185                 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
        195                 200                 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
    210                 215                 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
225                 230                 235                 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
                245                 250                 255
```

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
290 295 300

<210> 160
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 160
ggtgaaggca gaaattggag atg 23

<210> 161
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 161
atcccatgca tcagcctgtt tacc 24

<210> 162
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 162
gctggtgtag tctatacatc agatttgttt gctacacaag atcctcag 48

<210> 163
<211> 2076
<212> DNA
<213> Homo sapiens

<400> 163
cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60
tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaggtg 120

attgtttcgc tggtcctgtt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180
agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct caccccttac 240
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360
ttcttctggt tcttcccagc tcagatacag ccagaagatg ccccagtagt tctctggcta 420
cagggtgggc cgggaggttc atccatgttt ggactctttg tggaacatgg gccttatgtt 480
gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540
ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600
gcagtcaatg aggacgatgt agcacgggat ttatacagtg cactaattca gtttttccag 660
atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720
tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840
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aagcagtgcc atgaatgcat agaacacatc aggaagcaga actggtttga ggcctttgaa 960
atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020
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cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620
tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680
ttttgggggg agatgtttac tacaaaatta acatgagtac atgagtaaga attacattat 1740
ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800
ttttagggtc ttgaatagga agttttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860
taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920
gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980
ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040
gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164
<211> 476
<212> PRT
<213> Homo sapiens

<400> 164
Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

```
65                  70                  75                  80

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln
                85                  90                  95

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro
            100                 105                 110

Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val
        115                 120                 125

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
    130                 135                 140

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
145                 150                 155                 160

Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
                165                 170                 175

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu
            180                 185                 190

Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
        195                 200                 205

Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
    210                 215                 220

Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
225                 230                 235                 240

Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile
                245                 250                 255

Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His
            260                 265                 270

Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu
        275                 280                 285

Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
    290                 295                 300

Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
305                 310                 315                 320

Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
                325                 330                 335

Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly
            340                 345                 350
```

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
465 470 475

<210> 165
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 165
ttccatgcca cctaagggag actc 24

<210> 166
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 166
tggatgaggt gtgcaatggc tggc 24

<210> 167
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 167
agctctcaga ggctggtcat aggg 24

<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 168
gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac 50

<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens

<400> 169
cgagggcttt tccggctccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60
atttttccct ttcctaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120
tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180
tccttgcctc tctgtggata acagagcatg agaaagtgaa gagatgcagc ggagtgaggt 240
gatggaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300
cctggagagc ctgggggagg gcctgcctaa caagctttca aaaaacagga gcgacttcca 360
ctgggctggg ataagacgtg ccggtaggat agggaagact gggtttagtc ctaatatcaa 420
attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaaacgatgg 480
cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt 540
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gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
accaggatgg ggaccctggg tcaggccagc ctctttgctc ctcccggaaa ttatttttgg 720
tctgaccact ctgccttgtg ttttgcagaa tcatgtgagg gccaaccggg gaaggtggag 780
cagatgagca cacacaggag ccgtctcctc accgccgccc ctctcagcat ggaacagagg 840
cagccctggc cccgggccct ggaggtggac agccgctctg tggtcctgct ctcagtggtc 900
tgggtgctgc tggccccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960
aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020
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gaagtgctca ccctcaccaa caatgtcaac aagctgctca tcattgacta ctctgagaac 1200
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acgggcacca tgtacggggt gattgtgcgc tctgagggtg aggatggcaa gctcttcatc 1380
ggcacggctg tggatgggaa gcaggattac ttcccgaccc tgtccagccg gaagctgccc 1440
cgagaccctg agtcctcagc catgctcgac tatgagctac acagcgattt tgtctcctct 1500
ctcatcaaga tcccttcaga caccctggcc ctggtctccc actttgacat cttctacatc 1560
tacggctttg ctagtggggg ctttgtctac tttctcactg tccagcccga gacccctgag 1620
ggtgtggcca tcaactccgc tggagacctc ttctacacct cacgcatcgt gcggctctgc 1680

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gccttcaata tcaccagcca ggacgatgta ctctttgcca tcttctccaa agggcagaag 1860
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tggctgctgg ggaaggacgt ccagtgcacg aaggcgcctg tccccatcga tgataacttc 2040
tgtggactgg acatcaacca gcccctggga ggctcaactc cagtggaggg cctgaccctg 2100
tacaccacca gcagggaccg catgacctct gtggcctcct acgtttacaa cggctacagc 2160
gtggtttttg tggggactaa gagtggcaag ctgaaaaagg taagagtcta tgagttcaga 2220
tgctccaatg ccattcacct cctcagcaaa gagtccctct tggaaggtag ctattggtgg 2280
agatttaact ataggcaact ttattttctt ggggaacaaa ggtgaaatgg ggaggtaaga 2340
aggggttaat tttgtgactt agcttctagc tacttcctcc agccatcagt cattgggtat 2400
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acatctgcaa aagcaaa                                              2477

<210> 170
<211> 552
<212> PRT
<213> Homo sapiens

<400> 170
Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
  1               5                  10                  15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
             20                  25                  30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
         35                  40                  45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
     50                  55                  60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
 65                  70                  75                  80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
                 85                  90                  95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
            100                 105                 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
        115                 120                 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
    130                 135                 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
145                 150                 155                 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
                165                 170                 175
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Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
            180                 185                 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
        195                 200                 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
    210                 215                 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
225                 230                 235                 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
                245                 250                 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
            260                 265                 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
        275                 280                 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
    290                 295                 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
305                 310                 315                 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
                325                 330                 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
            340                 345                 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
        355                 360                 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
    370                 375                 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
385                 390                 395                 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
                405                 410                 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
            420                 425                 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
        435                 440                 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn
```

450 455 460

Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
465 470 475 480

Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
485 490 495

Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
500 505 510

Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
515 520 525

Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
530 535 540

Leu Tyr Phe Leu Gly Glu Gln Arg
545 550

<210> 171
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 171
tggaataccg cctcctgcag 20

<210> 172
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 172
cttctgccct ttggagaaga tggc 24

<210> 173
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 173
ggactcactg gcccaggcct tcaatatcac cagccaggac gat 42

<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1683)
<223> a, t, c or g

<400> 174
aggctcccgc gcgcggctga gtgcggactg gagtgggaac ccgggtcccc gcgcttagag 60
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120
tgctggtcgt cttgggcttc ctggtgctcc gcaggctgga ctggagcacc ctggtccctc 180
tgcggctccg ccatcgacag ctggggctgc aggccaaggg ctggaacttc atgctggagg 240
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ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggcccct 480
acatctgcag tgagatggac ctcgggggct tgcccagctg gctactccaa gaccctggca 540
tgaggctgag gacaacttac aagggcttca ccgaagcagt ggacctttat tttgaccacc 600
tgatgtccag ggtggtgcca ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660
tggagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720
cactggagga ccgtggcatt gtggaactgc tcctgacttc agacaacaag gatgggctga 780
gcaaggggat tgtccaggga gtcttggcca ccatcaactt gcagtcaaca cacgagctgc 840
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actggacggg gtggtttgac tcgtggggag gccctcacaa tatcttggat tcttctgagg 960
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atgaccagcg caaaggctta attggaaatc tctatctgaa tgattcaccc ctgaaaaact 1620
tcagaatcta tagcctggat atgaagaaga gcttctttca gaggttcggc ctggacaaat 1680
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tcaatggcca gaaccttgga cgttactgga acattggacc ccagaagacg ctttacctcc 1860
caggtccctg gttgagcagc ggaatcaacc aggtcatcgt ttttgaggag acgatggcgg 1920
gccctgcatt acagttcacg gaaacccccc acctgggcag gaaccagtac attaagtgag 1980
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ctggtggctg ctgccccacc cctcactgca aaagcatctc cttaagtagc aacctcaggg 2100
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ggatggctct gggcctggct ttgttgatga tggctttcct acagccctgc tcttgtgccg 2220
aggctgtcgg gctgtctcta gggtgggagc agctaatcag atcgcccagc ctttggccct 2280

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cagaaaaagt gctgaaacgt gcccttgcac cggacgtcac agccctgcga gcatctgctg 2340
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gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggcttg 3060
ggctcactgt cctgagttgc agtaaagcta taaccttgaa tcacaa                3106
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<210> 175
<211> 636
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (539)
<223> Any amino acid

<400> 175

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Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1               5                  10                  15

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
             20                  25                  30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
         35                  40                  45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
     50                  55                  60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
 65                  70                  75                  80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
                 85                  90                  95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
            100                 105                 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
        115                 120                 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
    130                 135                 140
```

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
145   150   155   160

Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
                165   170   175

His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
            180   185   190

Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
        195   200   205

Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
    210   215   220

Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
225   230   235   240

Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
                245   250   255

Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
            260   265   270

Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
        275   280   285

Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
    290   295   300

Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
305   310   315   320

Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
                325   330   335

Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
            340   345   350

Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
        355   360   365

Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
    370   375   380

Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
385   390   395   400

Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
                405   410   415

Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
            420   425   430

```
Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
        435                 440                 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
    450                 455                 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
465                 470                 475                 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
                485                 490                 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
            500                 505                 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
        515                 520                 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
    530                 535                 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
545                 550                 555                 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
                565                 570                 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
            580                 585                 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
        595                 600                 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
    610                 615                 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
625                 630                 635

<210> 176
<211> 2505
<212> DNA
<213> Homo sapiens

<400> 176
ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60
ccctggtgag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120
aaggggagca aagccgggct cggcccgagg cccccaggac ctccatctcc caatgttgga 180
ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgct gtaaacgcca 240
tggctcccaa gaagctgtcc tgccttcgtt ccctgctgct gccgctcagc ctgacgctac 300
tgctgcccca ggcagacact cggtcgttcg tagtggatag gggtcatgac cggtttctcc 360
tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420
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tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480
atgtgccctg gaactaccac gagccacagc ctggggtcta taactttaat ggcagccggg 540
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600
gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctggttg cttcgaaaac 660
ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720
aggtcttgct gcccaagata tatccatggc tttatcacaa tgggggcaac atcattagca 780
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ggagaattgc ttgaatccag gaggcagagg ttgcagtgag tggaggttgt accactgcac 2460
tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa                  2505
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<210> 177
<211> 654
<212> PRT
<213> Homo sapiens

<400> 177

```
Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
  1               5                  10                  15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
             20                  25                  30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
         35                  40                  45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
     50                  55                  60
```

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Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
 65                  70                  75                  80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
                 85                  90                  95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
            100                 105                 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
        115                 120                 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
    130                 135                 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
145                 150                 155                 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
                165                 170                 175

Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
            180                 185                 190

Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
        195                 200                 205

Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
    210                 215                 220

Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro
225                 230                 235                 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
                245                 250                 255

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr
            260                 265                 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
        275                 280                 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe
    290                 295                 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly
305                 310                 315                 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser
                325                 330                 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile
```

```
            340                 345                 350

Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro
        355                 360                 365

Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu
    370                 375                 380

Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu
385                 390                 395                 400

Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr
                405                 410                 415

Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val
            420                 425                 430

Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val
        435                 440                 445

Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr
    450                 455                 460

Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg
465                 470                 475                 480

Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro
                485                 490                 495

Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu
            500                 505                 510

Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys
        515                 520                 525

Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr
    530                 535                 540

Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly
545                 550                 555                 560

Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr
                565                 570                 575

Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu
            580                 585                 590

Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu
        595                 600                 605

Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu
    610                 615                 620
```

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
645 650

<210> 178
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 178
tggctactcc aagaccctgg catg 24

<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 179
tggacaaatc cccttgctca gccc 24

<210> 180
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 180
gggcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg 50

<210> 181
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 181
ccagctatga ctatgatgca cc 22

<210> 182
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 182
tggcacccag aatggtgttg gctc 24

<210> 183
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 183
cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184
<211> 1947
<212> DNA
<213> Homo sapiens

<400> 184
gctttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60
gcacccacaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattattt 120
gtgtttatgg ctttatctgc ctctacactc tcttctggtt attcaggata cctttgaagg 180
aatattcttt cgaaaaagtc agagaagaga gcagttttag tgacattcca gatgtcaaaa 240
acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300
ttggtgtgtt cttgtcagaa gttagtgaaa ataaacttag ggaaattagt ttgaaccatg 360
agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cgcccaggac aagcaggagt 420
tgcatctgtt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480
tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
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cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780
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cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttgttgtg gaagatcacc 1500
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aatgtttgta gggttttaag tcattcattt ccaaatcatt tttttttttc ttttggggaa 1800
agggaaggaa aaattataat cactaatctt ggttcttttt aaattgtttg taacttggat 1860
gctgccgcta ctgaatgttt acaaattgct tgcctgctaa agtaaatgat taaattgaca 1920
ttttcttact aaaaaaaaaa aaaaaaa                                     1947

<210> 185
<211> 501
<212> PRT
<213> Homo sapiens

<400> 185
Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
  1               5                  10                  15

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
             20                  25                  30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
         35                  40                  45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
     50                  55                  60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
 65                  70                  75                  80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
                 85                  90                  95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
            100                 105                 110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
        115                 120                 125

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
    130                 135                 140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
145                 150                 155                 160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
                165                 170                 175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
            180                 185                 190
```

```
Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
        195                 200                 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
    210                 215                 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
225                 230                 235                 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
                245                 250                 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
            260                 265                 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
        275                 280                 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
    290                 295                 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
305                 310                 315                 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
                325                 330                 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
            340                 345                 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
        355                 360                 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
    370                 375                 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
385                 390                 395                 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
                405                 410                 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
            420                 425                 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
        435                 440                 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
    450                 455                 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr
```

465 470 475 480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro
485 490 495

Phe Ala Asn Gly Ile
500

<210> 186
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 186
cctccctcta ttacccatgt c 21

<210> 187
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 187
gaccaacttt ctctgggagt gagg 24

<210> 188
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 188
gtcactttat ttctctaaca acaagctcga atccttacca gtggcag 47

<210> 189
<211> 2917
<212> DNA
<213> Homo sapiens

<400> 189
cccacgcgtc cggccttctc tctggacttt gcatttccat tccttttcat tgacaaactg 60
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aagacatttg tgttttacac acataaggat ctgtgtttgg ggtttcttct tcctcccctg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240
gcacttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300
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ggcctgaaag tgacacacag gcctgcatgt aaaaaaa 2917

<210> 190
<211> 607
<212> PRT
<213> Homo sapiens

<400> 190

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Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
 1               5                  10                  15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
            20                  25                  30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
        35                  40                  45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
    50                  55                  60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
65                  70                  75                  80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
                85                  90                  95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
            100                 105                 110

Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
        115                 120                 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
    130                 135                 140

Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
145                 150                 155                 160

Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
                165                 170                 175

Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
            180                 185                 190

Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
        195                 200                 205

Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
    210                 215                 220

Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
225                 230                 235                 240

Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
                245                 250                 255

Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
            260                 265                 270

Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
        275                 280                 285
```

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Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
    290                 295                 300

Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
305                 310                 315                 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
                325                 330                 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
            340                 345                 350

Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
        355                 360                 365

His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
    370                 375                 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
385                 390                 395                 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
                405                 410                 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
            420                 425                 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
        435                 440                 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
    450                 455                 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
465                 470                 475                 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
                485                 490                 495

Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
            500                 505                 510

Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
        515                 520                 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
    530                 535                 540

Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
545                 550                 555                 560

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val
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565 570 575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe
580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr
595 600 605

<210> 191
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 191
tctctattcc aaactgtggc g 21

<210> 192
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 192
tttgatgacg attcgaaggt gg 22

<210> 193
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 193
ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194
<211> 2362
<212> DNA
<213> Homo sapiens

<400> 194
gacggaagaa cagcgctccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60
cgggacatgc ggccccagga gctccccagg ctcgcgttcc cgttgctgct gttgctgttg 120
ctgctgctgc cgccgccgcc gtgccctgcc cacagcgcca cgcgcttcga ccccacctgg 180

gagtccctgg acgcccgcca gctgcccgcg tggtttgacc aggccaagtt cggcatcttc 240
atccactggg gagtgttttc cgtgcccagc ttcggtagcg agtggttctg gtggtattgg 300
caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagtttc 360
aaatatgaag attttggacc actatttaca gcaaaatttt ttaatgccaa ccagtgggca 420
gatatttttc aggcctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
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tttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920
cacacctaat gtgtatggta tagactgttg ctcctaggct acagacatat acagcatgtt 1980
actgaatact gtaggcaata gtaacagtgg tatttgtata tcgaaacata tggaaacata 2040
gagaaggtac agtaaaaata ctgtaaaata aatggtgcac ctgtataggg cacttaccac 2100
gaatggagct tacaggactg gaagttgctc tgggtgagtc agtgagtgaa tgtgaaggcc 2160
taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220
ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280
caaacgtttt aatttttaaa acctttttgg ctcttttgta ataacactta gcttaaaaca 2340
taaactcatt gtgcaaatgt aa 2362

<210> 195
<211> 467
<212> PRT
<213> Homo sapiens

<400> 195
Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
35 40 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
85 90 95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
180 185 190

Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
195 200 205

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
210 215 220

Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser
225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
450 455 460

Asn Val Ile
465

<210> 196
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 196
tggtttgacc aggccaagtt cgg 23

<210> 197
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 197
ggattcatcc tcaaggaaga gcgg 24

<210> 198

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 198
aacttgcagc atcagccact ctgc 24

<210> 199
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 199
ttccgtgccc agcttcggta gcgagtggtt ctggtggtat tggca 45

<210> 200
<211> 2372
<212> DNA
<213> Homo sapiens

<400> 200
agcagggaaa tccggatgtc tcggttatga agtggagcag tgagtgtgag cctcaacata 60
gttccagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120
catctgaggt gtttccctgg ctctgaaggg gtaggcacga tggccaggtg cttcagcctg 180
gtgttgcttc tcacttccat ctggaccacg aggctcctgg tccaaggctc tttgcgtgca 240
gaagagcttt ccatccaggt gtcatgcaga attatgggga tcacccttgt gagcaaaaag 300
gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360
ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420
ggctgggttg gagatggatt cgtggtcatc tctaggatta gcccaaaccc caagtgtggg 480
aaaaatgggg tgggtgtcct gatttggaag gttccagtga gccgacagtt tgcagcctat 540
tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaaa 600
gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgacagt 660
acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tcctcctgct 720
ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780
gaaactagca ccatgtctac agaaactgaa ccatttgttg aaaataaagc agcattcaag 840
aatgaagctg ctgggtttgg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900
tttggtgctg cagctggtct tggattttgc tatgtcaaaa ggtatgtgaa ggccttccct 960
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gccaatgata gcaaccctaa tgaggaatca aagaaaactg ataaaaaccc agaagagtcc 1080
aagagtccaa gcaaaactac cgtgcgatgc ctggaagctg aagtttagat gagacagaaa 1140
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atcaaaaggg ccaaagaacc aaagaagaaa gtccaccctt ggttcctaac tggaatcagc 1260
tcaggactgc cattggacta tggagtgcac caaagagaat gcccttctcc ttattgtaac 1320
cctgtctgga tcctatcctc ctacctccaa agcttcccac ggcctttcta gcctggctat 1380
gtcctaataa tatcccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440

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tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctaggtg ggttgaaagc 1500
caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac cctttcttca 1560
gctctgaaag agaaacacgt atcccacctg acatgtcctt ctgagcccgg taagagcaaa 1620
agaatggcag aaaagtttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680
tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacgacag tacactgtca 1740
gcagggactg taaacacaga cagggtcaaa gtgttttctc tgaacacatt gagttggaat 1800
cactgtttag aacacacaca cttacttttt ctggtctcta ccactgctga tattttctct 1860
aggaaatata ctttacaag taacaaaaat aaaaactctt ataaatttct atttttatct 1920
gagttacaga aatgattact aaggaagatt actcagtaat ttgtttaaaa agtaataaaa 1980
ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040
tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct gggaagctat 2100
ttttttcagt tttgatattt ctagcttatc tacttccaaa ctaattttta tttttgctga 2160
gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaagca cattttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca tttagaaaac tt                                2372
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<210> 201
<211> 322
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic protein

<400> 201

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Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
  1               5                  10                  15

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
             20                  25                  30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
         35                  40                  45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
     50                  55                  60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
 65                  70                  75                  80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
                 85                  90                  95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
            100                 105                 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
        115                 120                 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
    130                 135                 140
```

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Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
145                 150                 155                 160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
                165                 170                 175

Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
            180                 185                 190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
        195                 200                 205

Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
    210                 215                 220

Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
225                 230                 235                 240

Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
                245                 250                 255

Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
            260                 265                 270

Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
        275                 280                 285

Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
    290                 295                 300

Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
305                 310                 315                 320

Glu Val
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<210> 202
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 202
gagctttcca tccaggtgtc atgc 24

<210> 203
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 203
gtcagtgaca gtacctactc gg 22

<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 204
tggagcagga ggagtagtag tagg 24

<210> 205
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 205
aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt 50

<210> 206
<211> 1620
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (973)
<223> a, t, c or g

<220>
<221> modified_base
<222> (977)
<223> a, t, c or g

<220>
<221> modified_base
<222> (996)
<223> a, t, c or g

<220>
<221> modified_base

<222> (1003)
<223> a, t, c or g

<400> 206
agatggcggt cttggcacct ctaattgctc tcgtgtattc ggtgccgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccacccaacg cgaagacggt aacccgtgtg 180
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accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
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actttccttt gtgtggtagg acttggagga gaaatcccct ggactttcac taaccctctg 1560
acatactccc cacacccagt tgatggcttt ccgtaataaa aagattggga tttccttttg 1620

<210> 207
<211> 296
<212> PRT
<213> Homo sapiens

<400> 207
Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
 1   5   10   15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
            20   25   30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
        35   40   45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
    50   55   60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
65   70   75   80

```
Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
                85                  90                  95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
            100                 105                 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
        115                 120                 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
    130                 135                 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
145                 150                 155                 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
                165                 170                 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
            180                 185                 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
        195                 200                 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
    210                 215                 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
225                 230                 235                 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
                245                 250                 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
            260                 265                 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
        275                 280                 285

Asp Gly Glu Asn Lys Lys Asp Lys
    290                 295
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<210> 208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 208
gcttggatat tcgcatgggc ctac 24

<210> 209
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 209
tggagacaat atccctgagg 20

<210> 210
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 210
aacagttggc cacagcatgg cagg 24

<210> 211
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 211
ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212
<211> 1985
<212> DNA
<213> Homo sapiens

<400> 212
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tggggcccca gcctggcccg ggtcaccctg gcatgaggag atgggcctgt tgctcctggt 120
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aaaaa                                                             1985
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<210> 213
<211> 360
<212> PRT
<213> Homo sapiens

<400> 213

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Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
             20                  25                  30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
         35                  40                  45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
     50                  55                  60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
 65                  70                  75                  80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
                 85                  90                  95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
            100                 105                 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp
```

```
        115                 120                 125

Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr
    130                 135                 140

Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu
145                 150                 155                 160

Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg
                165                 170                 175

Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala
            180                 185                 190

Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly
        195                 200                 205

Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr
    210                 215                 220

Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro
225                 230                 235                 240

Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp
                245                 250                 255

Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu
            260                 265                 270

His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu
        275                 280                 285

Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys
    290                 295                 300

Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser
305                 310                 315                 320

Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu
                325                 330                 335

Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr
            340                 345                 350

Gly Val Tyr Cys Tyr Arg Gln His
        355                 360

<210> 214
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 214
tgcttcgcta ctgccctc 18

<210> 215
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 215
ttcccttgtg ggttggag 18

<210> 216
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 216
agggctggaa gccagttc 18

<210> 217
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 217
agccagtgag gaaatgcg 18

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 218
tgtccaaagt acacacacct gagg 24

<210> 219
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 219
gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220
<211> 1503
<212> DNA
<213> Homo sapiens

<400> 220
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tggccagggg agggtgcacc aggcggcccc cctgagcgac gctccccatg atgacgccca 180
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aaa 1503

<210> 221
<211> 328
<212> PRT
<213> Homo sapiens

<400> 221
Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Leu Arg His

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  1               5                  10                  15

Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly
            20                  25                  30

Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala
        35                  40                  45

His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val
    50                  55                  60

Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu
65                  70                  75                  80

Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp
                85                  90                  95

Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg
            100                 105                 110

His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp
        115                 120                 125

Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly
    130                 135                 140

His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr
145                 150                 155                 160

Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp
                165                 170                 175

Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu
            180                 185                 190

His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr
        195                 200                 205

Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu
    210                 215                 220

Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala
225                 230                 235                 240

Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn
                245                 250                 255

Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro
            260                 265                 270

Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu
        275                 280                 285
```

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
305 310 315 320

Leu Thr Arg His His Asp Glu Leu
325

<210> 222
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 222
cgcaggccct catggccagg 20

<210> 223
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 223
gaaatcctgg gtaattgg 18

<210> 224
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 224
gtgcgcggtg ctcacagctc atc 23

<210> 225
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 225
ccccccctgag cgacgctccc ccatgatgac gcccacggga actt 44

<210> 226
<211> 2403
<212> DNA
<213> Homo sapiens

<400> 226
ggggccttgc cttccgcact cgggcgcagc cgggtggatc tcgagcaggt gcggagcccc 60
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aaa 2403

<210> 227

<211> 550
<212> PRT
<213> Homo sapiens

<400> 227

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Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu
  1               5                  10                  15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
             20                  25                  30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
         35                  40                  45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
     50                  55                  60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
 65                  70                  75                  80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
                 85                  90                  95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
            100                 105                 110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
        115                 120                 125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
    130                 135                 140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
145                 150                 155                 160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
                165                 170                 175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
            180                 185                 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
        195                 200                 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
    210                 215                 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
225                 230                 235                 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
                245                 250                 255
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Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile
485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
530 535 540

Phe Leu Glu Ser Gln Gln
545 550

<210> 228
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 228
tggtctcgca caccgatc 18

<210> 229
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 229
ctgctgtcca caggggag 18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 230
ccttgaagca tactgctc 18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 231
gagatagcaa tttccgcc 18

<210> 232

<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 232
ttcctcaaga gggcagcc 18

<210> 233
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 233
cttggcacca atgtccgaga tttc 24

<210> 234
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 234
gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235
<211> 2586
<212> DNA
<213> Homo sapiens

<400> 235
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<210> 236
<211> 350
<212> PRT
<213> Homo sapiens

<400> 236

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Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
             20                  25                  30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
         35                  40                  45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
     50                  55                  60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
 65                  70                  75                  80
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Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
                 85                  90                  95

Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
            100                 105                 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
        115                 120                 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
    130                 135                 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145                 150                 155                 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
                165                 170                 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
            180                 185                 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
        195                 200                 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
    210                 215                 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225                 230                 235                 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
                245                 250                 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
            260                 265                 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
        275                 280                 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
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Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
305                 310                 315                 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
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<220>
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<400> 237
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<210> 238
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<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 238
ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 239
gcagagcgga gatgcagcgg cttg 24

<210> 240
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 240
ttggcagctt catggagg 18

<210> 241
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<212> DNA
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<400> 241
cctgggcaaa aatgcaac 18

<210> 242
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ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg 45

<210> 244
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<212> DNA
<213> Homo Sapien

<400> 244
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<210> 245
<211> 713
<212> PRT
<213> Homo Sapien

<400> 245

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				20				25						30	
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser	
				35				40						45	
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu	
				50				55						60	
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu	
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Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly	
				80				85						90	
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe	
				95				100						105	
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu	
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Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His	
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Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His	
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Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser
155 160 165

Asn Leu Leu Arg Leu His Leu Asn Ser Asn Leu Leu Arg Ala Ile
170 175 180

Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met
185 190 195

Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg
200 205 210

Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu
215 220 225

Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu
230 235 240

Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg
245 250 255

Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys
260 265 270

Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu
275 280 285

His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser
290 295 300

Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu
305 310 315

Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala
320 325 330

Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn
335 340 345

Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn
350 355 360

Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys
365 370 375

Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile
380 385 390

Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg
395 400 405

Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys

410 415 420

Leu Pro Leu Ile Ser Pro Arg Ser Phe Pro Pro Ser Leu Gln Val
425 430 435

Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu
440 445 450

Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu
455 460 465

Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly
470 475 480

Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr
485 490 495

Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val
500 505 510

Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu
515 520 525

Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His
530 535 540

Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn
545 550 555

Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr
560 565 570

Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr
575 580 585

Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala
590 595 600

Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr
605 610 615

Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly
620 625 630

Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly
635 640 645

Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly
650 655 660

Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser
665 670 675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
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Leu Pro Pro Leu Ser Gln Asn Ser
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<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 246
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<210> 247
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<400> 247
aaacttgtcg atggagacca gctc 24

<210> 248
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<400> 248
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<210> 249
<211> 3401
<212> DNA
<213> Homo Sapien

<400> 249
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<211> 546
<212> PRT
<213> Homo Sapien

<400> 250

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             20                  25                  30

Cys Thr Val Asp Ile Glu Ser Leu Thr Gly Tyr Arg Thr Tyr Arg
             35                  40                  45

Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe
             50                  55                  60

Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr
             65                  70                  75

Leu Trp Trp Met Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu
             80                  85                  90

Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys
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                 95                  100                 105

Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro
                110                 115                 120

Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu
                125                 130                 135

Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp
                140                 145                 150

Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu
                155                 160                 165

Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp
                170                 175                 180

Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val
                185                 190                 195

Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu
                200                 205                 210

Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala
                215                 220                 225

Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp
                230                 235                 240

Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu
                245                 250                 255

Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr
                260                 265                 270

Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu
                275                 280                 285

Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp

                290                 295                 300

Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr
                305                 310                 315

Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr
                320                 325                 330

Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser
                335                 340                 345

Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn
                350                 355                 360
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Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His
365 370 375

Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile
380 385 390

Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu
395 400 405

Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys
410 415 420

Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe
425 430 435

Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala
440 445 450

Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln
455 460 465

Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln
470 475 480

Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile
485 490 495

Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly
500 505 510

Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp
515 520 525

Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg
530 535 540

Ala Asp Lys Glu Gln Ala
545

<210> 251
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 251
caacaatgag ggcaccaagc 20

<210> 252
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 252
gatggctagg ttctggaggt tctg 24

<210> 253
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 253
caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254
<211> 1650
<212> DNA
<213> Homo Sapien

<400> 254
gcctgttgct gatgctgccg tgcggtactt gtcatggagc tggcactgcg 50

gcgctctccc gtcccgcggt ggttgctgct gctgccgctg ctgctgggcc 100

tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150

tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200

ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250

ggcttcaggg cggtccaggc ggttctagca ctggatttgg aaactttgag 300

gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350

ccaggctgcc agtctcctat ttgtggataa tcccgtgggc actgggttca 400

gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtggct 450

tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500

ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550

cagctggcat tggtctagag ctttataagg ccattcagcg agggaccatc 600

aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctcccctgt 650

tgattcggtg ctctcctggg gaccttacct gtacagcatg tctcttctcg 700

aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750

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agaaatgatc attgaacaga acacagatgg ggtgaacttc tataacatct 850

taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900

cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950

agatgcctta agccagctca tgaatggccc catcagaaag aagctcaaaa 1000

ttattcctga ggatcaatcc tggggaggcc aggctaccaa cgtctttgtg 1050

aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100

gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150

tcgtagatac catgggtcag gaggcctggg tgcggaaact gaagtggcca 1200

gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250

taaatctttg gaaacatctg cttttgtcaa gtcctacaag aaccttgctt 1300

tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350

atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400

gggctggaga tgagctggtt tggccttggg gcacagagct gagctgaggc 1450

cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500

gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550

ggaggcaatt tggaaattat ttctgcttct taaaaaaacc taagattttt 1600

taaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<210> 255
<211> 452
<212> PRT
<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
1					5					10					15
Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
				20					25					30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
				35					40					45	

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Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn
                 50                  55                  60

Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln
                 65                  70                  75

Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu
                 80                  85                  90

Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp
                 95                 100                 105

Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr
                110                 115                 120

Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu
                125                 130                 135

Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
                140                 145                 150

Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser
                155                 160                 165

Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu
                170                 175                 180

Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly
                185                 190                 195

Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
                200                 205                 210

Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys
                215                 220                 225

Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
                230                 235                 240

Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys
                245                 250                 255

Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr
                260                 265                 270

Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser
                275                 280                 285

Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His
                290                 295                 300

Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly
```

305 310 315

Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp
320 325 330

Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe
335 340 345

Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly
350 355 360

Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp
365 370 375

Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu
380 385 390

Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp
395 400 405

Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn
410 415 420

Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser
425 430 435

Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln
440 445 450

Gln Glu

<210> 256
<211> 1100
<212> DNA
<213> Homo Sapien

<400> 256
ggccgcggga gaggaggcca tgggcgcgcg cggggcgctg ctgctggcgc 50

tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100

ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150

tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctgggca 250

ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300

cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350

gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

cctcgctacc tggggaattc accctatgac attgccttgg tgaagctgtc 450

tgcacctgtc acctacacta aacacatcca gcccatctgt ctccaggcct 500

ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550

tacatcaaag aggatgaggc actgccatct ccccacaccc tccaggaagt 600

tcaggtcgcc atcataaaca actctatgtg caaccacctc ttcctcaagt 650

acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700

caaggcggga aggatgcctg cttcggtgac tcaggtggac ccttggcctg 750

taacaagaat ggactgtggt atcagattgg agtcgtgagc tggggagtgg 800

gctgtggtcg gcccaatcgg cccggtgtct acaccaatat cagccaccac 850

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tggggccggt ctgagcctac ctgagcccat gcagcctggg gccactgcca 1000

agtcaggccc tggttctctt ctgtcttgtt tggtaataaa cacattccag 1050

ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

<210> 257
<211> 314
<212> PRT
<213> Homo Sapien

<400> 257

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg
1 5 10 15

Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser
20 25 30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly
35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
50 55 60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
65 70 75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
80 85 90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
95 100 105

Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
110 115 120

Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
125 130 135

Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
140 145 150

Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
155 160 165

Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
170 175 180

Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
185 190 195

Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
200 205 210

Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
215 220 225

Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
230 235 240

Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
245 250 255

Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
260 265 270

Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
275 280 285

Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
290 295 300

Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
305 310

<210> 258
<211> 2427
<212> DNA
<213> Homo Sapien

<400> 258
cccacgcgtc cgcggacgcg tgggaagggc agaatgggac tccaagcctg 50

cctcctaggg ctctttgccc tcatcctctc tggcaaatgc agttacagcc 100

cggagcccga ccagcggagg acgctgcccc caggctgggt gtccctgggc 150

cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200

gaatgtggaa agactctcgg agctggtgca ggctgtgtcg gatcccagct 250

ctcctcaata cggaaaatac ctgaccctag agaatgtggc tgatctggtg 300

aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350

cggagcccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400

ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagtttcat 450

cactatgtgg gaggacctac ggaaacccat gttgtaaggt ccccacatcc 500

ctaccagctt ccacaggcct tggcccccca tgtggacttt gtggggggac 550

tgcaccgttt tcccccaaca tcatccctga ggcaacgtcc tgagccgcag 600

gtgacaggga ctgtaggcct gcatctgggg gtaacccccc ctgtgatccg 650

taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700

acagccaagc ctgtgcccag ttcctggagc agtatttcca tgactcagac 750

ctggctcagt tcatgcgcct cttcggtggc aactttgcac atcaggcatc 800

agtagcccgt gtggttggac aacagggccg gggccgggcc gggattgagg 850

ccagtctaga tgtgcagtac ctgatgagtg ctggtgccaa catctccacc 900

tgggtctaca gtagccctgg ccggcatgag ggacaggagc ccttcctgca 950

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tatcagtggt ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300

aggaagctgt aacgaagttc ctgagctcta gcccccacct gccaccatcc 1350

agttacttca atgccagtgg ccgtgcctac ccagatgtgg ctgcactttc 1400

tgatggctac tgggtggtca gcaacagagt gcccattcca tgggtgtccg 1450

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gtcccctgcc ctgaagctgg cagttcagtc ccttattctg ccctgttgga 1800

agccctgctg aaccctcaac tattgactgc tgcagacagc ttatctccct 1850

aaccctgaaa tgctgtgagc ttgacttgac tcccaaccct accatgctcc 1900

atcatactca ggtctcccta ctcctgcctt agattcctca ataagatgct 1950

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tgtagatttt tgctcttctc agtttactca ttgtcccctg gaacaaatca 2350

ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400

aatgattgat acctcaaatg taaaaaa 2427

<210> 259
<211> 556
<212> PRT
<213> Homo Sapien

<400> 259
Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu
1 5 10 15

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

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                  20                  25                  30

Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu
                  35                  40                  45

Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg
                  50                  55                  60

Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln
                  65                  70                  75

Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg
                  80                  85                  90

Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala
                  95                 100                 105

Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu
                 110                 115                 120

Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly
                 125                 130                 135

Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val
                 140                 145                 150

Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro
                 155                 160                 165

His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser
                 170                 175                 180

Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly
                 185                 190                 195

Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn
                 200                 205                 210

Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln
                 215                 220                 225

Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu
                 230                 235                 240

Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala
                 245                 250                 255

Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly
                 260                 265                 270

Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala
                 275                 280                 285
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Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly
                290                 295                 300

Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser
                305                 310                 315

Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp
                320                 325                 330

Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met
                335                 340                 345

Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp
                350                 355                 360

Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg
                365                 370                 375

Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly
                380                 385                 390

Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp
                395                 400                 405

Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser
                410                 415                 420

Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His
                425                 430                 435

Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro
                440                 445                 450

Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg
                455                 460                 465

Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val
                470                 475                 480

Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser
                485                 490                 495

Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln
                500                 505                 510

His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser
                515                 520                 525

Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro
                530                 535                 540

Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu
                545                 550                 555
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Cys

<210> 260
<211> 1638
<212> DNA
<213> Homo Sapien

<400> 260
gccgcgcgct ctctcccggc gcccacacct gtctgagcgg cgcagcgagc 50

cgcggcccgg gcgggctgct cggcgcggaa cagtgctcgg catggcaggg 100

attccagggc tcctcttcct tctcttcttt ctgctctgtg ctgttgggca 150

agtgagccct tacagtgccc cctggaaacc cacttggcct gcataccgcc 200

tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250

ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300

taagggaact ccactgccca cttacgaaga ggccaagcaa tatctgtctt 350

atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400

tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450

ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500

tcagcatttt tgggaaggac ttcctgctca actacccttt ctcaacatca 550

gtgaagttat ccacgggctg caccggcacc ctggtggcag agaagcatgt 600

cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 650

cccagaagct tcgagtgggc ttcctaaagc ccaagtttaa agatggtggt 700

cgaggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750

gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800

atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850

aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctcctgctaa 900

gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950

caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000

ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctggggt 1050

ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100

ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150

gatttcaacg tggctgtcag aatcactcct ctcaaatatg cccagatttg 1200

ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250

ttccctcctg gcagcaatta agggtcttca tgttcttatt ttaggagagg 1300

ccaaattgtt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350

tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400

tgactggctt tactatttga aaactggttt gtgtatcata tcatatatca 1450

tttaagcagt ttgaaggcat acttttgcat agaaataaaa aaaatactga 1500

tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550

caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600

atatttggca tacaagagat atgaaaaaaa aaaaaaaa 1638

<210> 261
<211> 383
<212> PRT
<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu	
1				5				10						15	
Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro	
				20				25						30	
Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr	
				35				40						45	
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu	
				50				55						60	
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu	
				65				70						75	
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu	
				80				85						90	
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile	
				95				100						105	
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser	
				110				115						120	

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Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser
                125                 130                 135

Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe
            140                 145                 150

Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val
            155                 160                 165

Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
            170                 175                 180

Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu
            185                 190                 195

Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr
            200                 205                 210

Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys
            215                 220                 225

Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
            230                 235                 240

Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro
            245                 250                 255

His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys
            260                 265                 270

Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
            275                 280                 285

Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu
            290                 295                 300

Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala
            305                 310                 315

Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln
            320                 325                 330

Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp
            335                 340                 345

Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg
            350                 355                 360

Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly
            365                 370                 375

Asn Tyr Leu Asp Cys Arg Glu Gly
            380
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<210> 262
<211> 1378
<212> DNA
<213> Homo Sapien

<400> 262
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ccatggtggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100

accttcacct ccctgctgct gctggcgtcg acagccatcc tcaatgcggc 150

caggatacct gttcccccag cctgtgggaa gccccagcag ctgaaccggg 200

ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250

atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 300

ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350

acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400

cggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450

ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctcgagcgct 500

ccatacagtt ctcagagcgg gtcctgccca tctgcctacc tgatgcctct 550

atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600

ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650

ttcctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700

ggacagggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750

ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800

tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850

gccgagcgca acaggcccgg ggtctacatc agcctctctg cgcaccgctc 900

ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950

ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000

tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050

cacatctgga tctggatctg cggcggcctc gggcggtttc ccccgccgta 1100

aataggctca tctacctcta cctctggggg cccggacggc tgctgcggaa 1150

aggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200

catcaggccc cgcccaacgg cctcatgtcc ccgcccccac gacttccggc 1250

cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300

ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350

ataaattatt tattctccaa aaaaaaaa 1378

<210> 263
<211> 317
<212> PRT
<213> Homo Sapien

<400> 263

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu
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Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu
20 25 30

Asn Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln
35 40 45

Gln Leu Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu
50 55 60

Trp Pro Trp Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys
65 70 75

Ala Gly Ser Leu Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His
80 85 90

Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu
95 100 105

Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser Gln Lys
110 115 120

Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys
125 130 135

Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser
140 145 150

Ile Gln Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala
155 160 165

Ser Ile His Leu Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp
170 175 180

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
185 190 195

Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
200 205 210

Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
215 220 225

Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
230 235 240

Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
245 250 255

Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
260 265 270

Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
275 280 285

Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
290 295 300

Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala
305 310 315

Arg Ser

<210> 264
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 264
gtccgcaagg atgcctacat gttc 24

<210> 265
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 265
gcagaggtgt ctaaggttg 19

<210> 266
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 267
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 268
ggggaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
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<220>
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<400> 271
gcggaagggc agaatgggac tccaag 26

<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45

<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gccctcatcc tctctggcaa atgcagttac agcccggagc ccgac 45

<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
gggcagggat tccagggctc c 21

<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgcatt gctggtagag caag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280
ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 281
cgtctcgagc gctccataca gttcccttgc ccca 34

<210> 282
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 282
tggaggggga gcgggatgct tgtctgggcg actccggggg ccccctcatg 50

tgccaggtgg a 61

<210> 283
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 283
ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284
<211> 1875
<212> DNA
<213> Homo Sapien

<400> 284
gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgtttga tggtggagct gcacaacctc taccgggccc 150

aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200

ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250

caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300

gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350

tacaacctca gcgccgccac ctgcagccca ggccagatgt gcggccacta 400

cacgcaggtg gtatgggcca agacagagag gatcggctgt ggttcccact 450

tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500

tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550

ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600

tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650

gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700

aatgggtact ccttcttccc tagcaacggg gattccggct ttcttggtaa 750

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ggctccacct tgcgtaacaa ctgaggtccc ttccattttg gcagctcaca 900

gcctgccctc cttggatgag gagccagtta ccttccccaa atcgacccat 950

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ttgcctcctt ccagtgaggt cttggcctca gtttttccag cccaggacaa 1150

gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200

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caagcctagc gttgtgtcag ggctgaactc gggccctggt catgtgtggg 1350

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ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550

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ggactgcaca ccgggcccac acctctcctg cccctccctc ctgagtcctg 1650

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tgcccacaca gcatgtgcgc tctccctgag tgcctgtgta gctggggatg 1750

gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800

tgagtggggg aggcagggac gagggaagga aagtaactcc tgactctcca 1850

ataaaaacct gtccaacctg tgaaa 1875

<210> 285
<211> 463
<212> PRT
<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu	
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Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp	
				20				25						30	
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala	
				35				40						45	
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp	
				50				55						60	
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val	
				65				70						75	
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe	
				80				85						90	
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu	
				95				100						105	
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys	
				110				115						120	
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	
				125				130						135	

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu
140 145 150

Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr
155 160 165

Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly
170 175 180

Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser
185 190 195

Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro
200 205 210

Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser
215 220 225

Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile
230 235 240

Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys
245 250 255

Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr
260 265 270

Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr
275 280 285

Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu
290 295 300

Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
305 310 315

Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
320 325 330

Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly
335 340 345

Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu
350 355 360

Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
365 370 375

Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr
380 385 390

Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
395 400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
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Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
455 460

<210> 286
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 286
tcctgcagtt tcctgatgc 19

<210> 287
<211> 24
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 287
ctcatattgc acaccagtaa ttcg 24

<210> 288
<211> 45
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 288
atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289
<211> 3662
<212> DNA
<213> Homo Sapien

<400> 289
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caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200

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ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550

aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttgg 600

tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650

atggagcttt ttgggggctg agcaacatgg aaattttgca gctggaccat 700

aacaacctaa cagagattac caaaggctgg ctttacggct tgctgatgct 750

gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800

cctgggagtt ctgccagaag ctcagtgagc tggacctaac tttcaatcac 850

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gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100

tcactggttt ggatgcattg gagcatctag acctgagtga caacgcaatc 1150

atgtctttac aaggcaatgc attttcacaa atgaagaaac tgcaacaatt 1200

gcatttaaat acatcaagcc ttttgtgcga ttgccagcta aaatggctcc 1250

cacagtgggt ggcggaaaac aactttcaga gctttgtaaa tgccagttgt 1300

gcccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350

tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400

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gccagcagca gtgattcccc aatgactttt gcttggaaaa aagacaatga 1500

actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggcccaag 1550

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tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150

agattttcag gaagaaaatc acatttgtac ctttaaacag actttagaaa 3200

actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250

tgagaccaaa ggaaaagctt aacatactac ctcaagtgaa cttttattta 3300

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<400> 290

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Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys	
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Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
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Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
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Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
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Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
                 80                  85                  90

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
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Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
                110                 115                 120

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
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Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
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Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

                155                 160                 165

Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
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Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
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Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
                200                 205                 210

Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
                215                 220                 225

Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
                230                 235                 240

Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
                245                 250                 255

Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
                260                 265                 270

Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn
                275                 280                 285

Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser
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290 295 300

Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile
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Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg
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Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala
335 340 345

Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn
350 355 360

Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys
365 370 375

Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys
380 385 390

Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln
395 400 405

Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly
410 415 420

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp
425 430 435

Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala
440 445 450

Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser
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Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu

470 475 480

Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln
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Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu
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Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn
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His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn
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Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg
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Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
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Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
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Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
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Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
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Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
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Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
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Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
665 670 675

Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
680 685 690

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
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Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
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Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
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Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
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Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
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Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
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Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
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Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
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Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
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Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
830 835 840

Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
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Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
860 865 870

Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
875 880 885

Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
890 895 900

Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
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Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
920 925 930

Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
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Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
950 955 960

Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
965 970 975

Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
980 985 990

Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
995 1000 1005

Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
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Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
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Asn Phe Gln Ser Tyr Asp Leu Asp Thr
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<212> PRT
<213> Homo Sapien

<400> 292

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				20				25						30	
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln	
				35				40						45	
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val	
				50				55						60	
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser	
				65				70						75	
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile	
				80				85						90	
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu	
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Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe	
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Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg	
				125				130						135	
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu	
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Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser	

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Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly
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Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp
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Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln
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Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile
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Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val
                260                 265                 270

Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp
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Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His
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Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp
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Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys
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Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp
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Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro
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Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys
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Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn
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Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val
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Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp
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Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
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Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro
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Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
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Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
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Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
485 490 495

Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
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Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
515 520 525

Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
530 535 540

Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
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Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
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Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
575 580 585

Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
590 595 600

Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn
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Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn
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Ser Lys Asp Asn Val Gln Glu Thr Gln Ile
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<213> Homo Sapien

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  1               5                  10                  15

Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly
                20                  25                  30

Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg
                35                  40                  45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
                50                  55                  60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp
                65                  70                  75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
                80                  85                  90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
                95                 100                 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
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Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
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Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
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Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
               155                 160                 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
               170                 175                 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
               185                 190                 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
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Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
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                215                 220                 225

Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
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Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
                245                 250                 255

Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
                260                 265                 270

Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
                275                 280                 285

Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
                290                 295                 300

Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
                305                 310                 315

Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
                320                 325                 330

Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn
                335                 340                 345

Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser
                350                 355                 360

Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile
                365                 370                 375

Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg
                380                 385                 390

Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala
                395                 400                 405

Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn
                410                 415                 420

Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys
                425                 430                 435

Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys
                440                 445                 450

Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln
                455                 460                 465

Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly
                470                 475                 480
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Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp
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Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala
                500                 505                 510

Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser
                515                 520                 525

Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu
                530                 535                 540

Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln
                545                 550                 555

Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu
                560                 565                 570

Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn
                575                 580                 585

His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn
                590                 595                 600

Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg
                605                 610                 615

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
                620                 625                 630

Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
                635                 640                 645

Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
                650                 655                 660

Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
                665                 670                 675

Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
                680                 685                 690

Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
                695                 700                 705

Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
                710                 715                 720

Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
                725                 730                 735

Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
                740                 745                 750
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Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
755 760 765

Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
770 775 780

Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
785 790 795

Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
800 805 810

Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
815 820 825

Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
830 835 840

Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
845 850 855

Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
860 865 870

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
875 880 885

Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
890 895 900

Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
905 910 915

Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
920 925 930

Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
935 940 945

Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
950 955 960

Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
965 970 975

Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
980 985 990

Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
995 1000 1005

Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu

1010 1015 1020

Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
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Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
1040 1045 1050

Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
1055 1060 1065

Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
1070 1075 1080

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
1085 1090 1095

His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
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Asn Phe Gln Ser Tyr Asp Leu Asp Thr
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<210> 296
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<212> DNA
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<400> 296
cctaaactga actggacca 19

<210> 297
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<212> DNA
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<400> 297
ggctggagac actgaacct 19

<210> 298
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acagctgcac agctcagaac agtg 24

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gggtcttggt gaatgagg 18

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<400> 304

ccccatgtgt ccatgactgt tccc 24

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ttagcagctg aggatgggca caac 24

<210> 308
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<210> 309
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<400> 309
gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310
<211> 3296
<212> DNA
<213> Homo Sapien

<400> 310

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cgagcccgcg gagcgcagct gagactgggg gagcgcgttc ggcctgtggg 100

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ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtggtc 200

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<210> 314
<211> 3003
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<213> Homo Sapien

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aat 3003

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<212> PRT
<213> Homo Sapien

<400> 315

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35 40 45

Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
50 55 60

Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
65 70 75

Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
80 85 90

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
95 100 105

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
110 115 120

Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
125 130 135

Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg
140 145 150

Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
155 160 165

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
170 175 180

Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
185 190 195

Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
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Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
215 220 225

Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
230 235 240

Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr
245 250 255

Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
260 265 270

Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
275 280 285

Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro
290 295 300

Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr
305 310 315

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Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr
335 340 345

Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala
350 355 360

Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln
365 370 375

Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val
380 385 390

His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu
395 400 405

Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly

410 415 420

Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys

425 430 435

Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly
440 445 450

Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser
455 460 465

Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala
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<223> Synthetic Oligonucleotide Probe

<400> 316
gatggttcct gctcaagtgc cctg 24

<210> 317
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 317
ttgcacttgt aggacccacg tacg 24

<210> 318
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 318
ctgatgggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319
<211> 2110
<212> DNA

<213> Homo Sapien

<400> 319

cttctttgaa aaggattatc acctgatcag gttctctctg catttgcccc 50

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caacaggtgc ttgctcgggg ctgaaggtga cagtgccatc acacactgtc 150

catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200

cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250

caatgcccaa atacttactg ggctctgtga ataagtctgt ggttcctgac 300

ttggaatacc aacacaagtt caccatgatg ccacccaatg catctctgct 350

tatcaaccca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400

acattcaggg aaatggaact ctatctgcca gtcagaagat acaagtcacg 450

gttgatgatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500

ggctgtggag tatgtgggga acatgaccct gacatgccat gtggaagggg 550

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agctccacct actccttttc tccccaaaac aatacccttc atattgctcc 650

agtaaccaag gaagacattg ggaattacag ctgcctggtg aggaaccctg 700

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atcccccaa cacctactcc tggattagga ggactgacaa tactacatat 900

atcattaagc atgggcctcg cttagaagtt gcatctgaga aagtagccca 950

gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000

aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050

cttgcacaga aaggaaaatc attgtcacct ttagcaagta taactggaat 1100

atcactattt ttgattatat ccatgtgtct tctcttccta tggaaaaaat 1150

atcaacccta caaagttata aaacagaaac tagaaggcag gccagaaaca 1200

gaatacagga aagctcaaac attttcaggc catgaagatg ctctggatga 1250

cttcggaata tatgaatttg ttgcttttcc agatgtttct ggtgtttcca 1300

ggattccaag caggtctgtt ccagcctctg attgtgtatc ggggcaagat 1350

ttgcacagta cagtgtatga agttattcag cacatccctg cccagcagca 1400

agaccatcca gagtgaactt tcatgggcta aacagtacat tcgagtgaaa 1450

ttctgaagaa acattttaag gaaaaacagt ggaaaagtat attaatctgg 1500

aatcagtgaa gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550

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tggaaacttt acattgttcg atttttcagc agactttgtt ttattaaatt 1850

tttattagtg ttaagaatgc taaatttatg tttcaatttt atttccaaat 1900

ttctatcttg ttatttgtac aacaaagtaa taaggatggt tgtcacaaaa 1950

acaaaactat gccttctctt ttttttcaat caccagtagt attttgaga 2000

agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050

tttcaaggaa agatggattc aaataaatta ttctgttttt gcttttaaaa 2100

aaaaaaaaaa 2110

<210> 320
<211> 450
<212> PRT
<213> Homo Sapien

<400> 320

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Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His	
				20				25						30	
Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe	
				35				40						45	
His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg	
				50				55						60	

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
65 70 75

Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
80 85 90

Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
95 100 105

Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
110 115 120

Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
125 130 135

Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
140 145 150

Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
155 160 165

Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
170 175 180

Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
185 190 195

Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
200 205 210

Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
215 220 225

Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
230 235 240

Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu
245 250 255

Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp
260 265 270

Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro
275 280 285

Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp
290 295 300

Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu
305 310 315

Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

320 325 330

Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly
335 340 345

Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp
350 355 360

Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly
365 370 375

Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His
380 385 390

Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe
395 400 405

Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro
410 415 420

Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr
425 430 435

Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu
440 445 450

<210> 321
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 321
gatcctgtca caaagccagt ggtgc 25

<210> 322

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 322
cactgacagg gttcctcacc cagg 24

<210> 323
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 323
ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324
<211> 2397
<212> DNA
<213> Homo Sapien

<400> 324
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cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100

acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aattttatgc cccgtggtgc cctgcttgtc aaaatcttca 200

accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250

ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatc 300

ataactgctc ttcctactat ttatcattgt aaagatggtg aatttaggcg 350

ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtgata 400

aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450

gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500

gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550

catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600

ctctgtatga tatttgtggc agattgcctt tgtccttcaa aaaggcgcag 650

accacagcca tacccatacc cttcaaaaaa attattatca gaatctgcac 700

aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750

tcagaagaag aagctgaaag taaagaagga acaaacaaag actttccaca 800

gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850

cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900

aagattgatc attttgtttg gtttgaagtg aactgtgact tttttgaata 950

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acataaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050

gatggtttaa atagttctct aatttttgaa aaatcgtgcc aagcaataag 1100

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aatttacatt tcccaagtat tgcattattg aggtatttaa gaagattatt 1200

ttagagaaaa atatttctca tttgatataa tttttctctg tttcactgtg 1250

tgaaaaaaag aagatatttc ccataaatgg gaagtttgcc cattgtctca 1300

agaaatgtgt atttcagtga caatttcgtg gtctttttag aggtatattc 1350

caaaatttcc ttgtattttt aggttatgca actaataaaa actaccttac 1400

attaattaat tacagttttc tacacatggt aatacaggat atgctactga 1450

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attttctctt gtatttttct tacttactat gggttacatt ttttatttt 1550

caaattggat gataatttct tggaaacatt ttttatgttt tagtaaacag 1600

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aacaatctgt tgtaatttaa aattttggcc actttttca gattttacat 1700

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atacagaaag ttcttaattg attttacagt ctgtaatgct tgatgtttta 1950

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tgttctttcc tgactggtaa tattgtgtgg gatttcacag gtaaaagtca 2050

gtaggatgga acattttagt gtatttttac tccttaaaga gctagaatac 2100

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tctgttgctg tgtgaatcca ttagatttac agtatcgtaa tatacaagtt 2250

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aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaa 2397

<210> 325
<211> 280
<212> PRT

<213> Homo Sapien

<400> 325
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Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn
                20   25   30

Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly
                35   40   45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln
                50   55   60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
                65   70   75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly
                80   85   90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
                95   100   105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys
                110   115   120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile
                125   130   135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser
                140   145   150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys
                155   160   165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser
                170   175   180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
                185   190   195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
                200   205   210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

215 220 225

Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
230 235 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu
245 250 255

Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser
260 265 270

Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser
275 280

<210> 326
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 326
tgaggtgggc aagcggcgaa atg 23

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 327
tatgtggatc aggacgtgcc 20

<210> 328
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 328
tgcagggttc agtctagatt g 21

<210> 329
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 329
ttgaaggaca aaggcaatct gccac 25

<210> 330
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 330
ggagtcttgc agttcccctg gcagtcctgg tgctgttgct ttggg 45

<210> 331
<211> 2168
<212> DNA
<213> Homo Sapien

<400> 331
gcgagtgtcc agctgcggag acccgtgata attcgttaac taattcaaca 50

aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taacccagtg 100

ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150

acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200

ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250

cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300

agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350

ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400

tacctggctc accctgtgaa tgcctacaaa ctggtgaagc ggctaaacac 450

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gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600

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caatgctgag tgtggatgac tgctttggga tgggccgctc ggcctacaat 700

gaaggggact attatcatac ggtgttgtgg atggagcagg tgctaaagca 750

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taccgggttt ccaaaagctc ctggctagag gaagatgatg accctgttgt 1350

ggcccgagta aatcgtcgga tgcagcatat cacagggtta acagtaaaga 1400

ctgcagaatt gttacaggtt gcaaattatg gagtgggagg acagtatgaa 1450

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ggtacagctg tgttctggta caacctcttg cggagcgggg aaggtgacta 1650

ccgaacaaga catgctgcct gccctgtgct tgtgggctgc aagtgggtct 1700

ccaataagtg gttccatgaa cgaggacagg agttcttgag accttgtgga 1750

tcaacagaag ttgactgaca tccttttctg tccttcccct tcctggtcct 1800

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gcctgtgcca tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000

gttagctgtc tagcgcctag caaggtgcct ttgtacctca ggtgttttag 2050

gtgtgagatg tttcagtgaa ccaaagttct gataccttgt ttacatgttt 2100

gtttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaa 2168

<210> 332
<211> 533
<212> PRT
<213> Homo Sapien

<400> 332

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             20                  25                  30

Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys
             35                  40                  45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser
             50                  55                  60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp
             65                  70                  75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val
             80                  85                  90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu
             95                 100                 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg
            110                 115                 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala
            125                 130                 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile
            140                 145                 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser
            155                 160                 165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly
            170                 175                 180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln
            185                 190                 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu
            200                 205                 210
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Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg
215 220 225

Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His
230 235 240

Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu
245 250 255

Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu
260 265 270

Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro
275 280 285

Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys
290 295 300

Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His
305 310 315

Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu
320 325 330

Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met
335 340 345

Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys
350 355 360

Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr
365 370 375

Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp
380 385 390

Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile
395 400 405

Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn
410 415 420

Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg
425 430 435

Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala
440 445 450

Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr
455 460 465

Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr
470 475 480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp
530

<210> 333
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 333
ccaggcacaa tttccaga 18

<210> 334
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<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 334
ggacccttct gtgtgccag 19

<210> 335
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 335
ggtctcaaga actcctgtc 19

<210> 336
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta cttg 24

<210> 337
<211> 45
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 337
gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338
<211> 2789

<212> DNA
<213> Homo Sapien

<400> 338
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tcccagtgtg agtgaaattg attgtttcat ttattaccgt tttggctggg 100

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agacaggaca atcttcttgg ggatgctggt cctggaagcc agcgggcctt 200

gctctgtctt tggcctcatt gaccccaggt tctctggtta aaactgaaag 250

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cccgggctcc agcagggatg caggtggtgt ctcatgggga tgagcggccc 800

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cgactacgac tggttcttca tcatgcagga tgacacatat gtgcaggccc 900

cccgcctggc agcccttgct ggccacctca gcatcaacca agacctgtac 950

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tcatgggggc tttggctacc tgttgtcacg gagtctcctg cttcgtctgc 1050

ggccacatct ggatggctgc cgaggagaca ttctcagtgc ccgtcctgac 1100

gagtggcttg gacgctgcct cattgactct ctgggcgtcg gctgtgtctc 1150

acagcaccag gggcagcagt atcgctcatt tgaactggcc aaaaataggg 1200

accctgagaa ggaagggagc tcggctttcc tgagtgcctt cgccgtgcac 1250

cctgtctccg aaggtaccct catgtaccgg ctccacaaac gcttcagcgc 1300

tctggagttg gagcgggctt acagtgaaat agaacaactg caggctcaga 1350

tccggaacct gaccgtgctg acccccgaag gggaggcagg gctgagctgg 1400

cccgttgggc tccctgctcc tttcacacca cactctcgct ttgaggtgct 1450

gggctgggac tacttcacag agcagcacac cttctcctgt gcagatgggg 1500

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caccctgttg ctggtctacg ggccacgaga aggtggccgt ggagctccag 1950

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tgtcgcatga atgccatctc tggctggcag gccttctttc cagtccattt 2200

ccaggagttc aatcctgccc tgtcaccaca gagatcaccc ccagggcccc 2250

cgggggctgg ccctgacccc ccctcccctc ctggtgctga cccctcccgg 2300

ggggctccta taggggggag atttgaccgg caggcttctg cggagggctg 2350

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gttttcctcc ggttctcagg gctccacctc tttcgggccg tagagccagg 2500

gctggtgcag aagttctccc tgcgagactg cagcccacgg ctcagtgaag 2550

aactctacca ccgctgccgc ctcagcaacc tggaggggct aggggccgt 2600

gcccagctgg ctatggctct ctttgagcag gagcaggcca atagcactta 2650

gcccgcctgg gggccctaac ctcattacct ttcctttgtc tgcctcagcc 2700

ccaggaaggg caaggcaaga tggtggacag atagagaatt gttgctgtat 2750

tttttaaata tgaaaatgtt attaaacatg tcttctgcc 2789

<210> 339
<211> 772
<212> PRT
<213> Homo Sapien

<400> 339

Met Arg Leu Ser Ser Leu Leu Ala Leu Leu Arg Pro Ala Leu Pro
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Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg
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Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala
35 40 45

Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
50 55 60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
65 70 75

Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg
80 85 90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

95 100 105

Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val
110 115 120

Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr
125 130 135

Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser
140 145 150

His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg
155 160 165

His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile
170 175 180

Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu
185 190 195

Ala Gly His Leu Ser Ile Asn Gln Asp Leu Tyr Leu Gly Arg Ala
200 205 210

Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg Tyr Cys His Gly
215 220 225

Gly Phe Gly Tyr Leu Leu Ser Arg Ser Leu Leu Leu Arg Leu Arg
230 235 240

Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro
245 250 255

Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly
260 265 270

Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu
275 280 285

Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu
290 295 300

Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr
305 310 315

Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr
320 325 330

Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val
335 340 345

Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu
350 355 360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp
365 370 375

Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala
380 385 390

Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp
395 400 405

Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro
410 415 420

Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg
425 430 435

Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu
440 445 450

Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg
455 460 465

Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met
470 475 480

Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu
485 490 495

Leu Val Ala Glu Ala Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe
500 505 510

Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu
515 520 525

Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp
530 535 540

Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg
545 550 555

Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala
560 565 570

Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro
575 580 585

Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly
590 595 600

Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp
605 610 615

Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu
620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
635 640 645

Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
650 655 660

Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
665 670 675

Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
680 685 690

Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
695 700 705

Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
710 715 720

Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
725 730 735

Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
740 745 750

Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
755 760 765

Gln Glu Gln Ala Asn Ser Thr
770

<210> 340
<211> 1572
<212> DNA
<213> Homo Sapien

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tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100

ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150

tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200

catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250

ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300

ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350

accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gtttgagtca attaatatgg acacaaatga catgtggtta atgatgagaa 450

aagcttacaa atacgccttt gataagtata gagaccaata caactggttc 500

ttccttgcac gccccactac gtttgctatc attgaaaacc taaagtattt 550

tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600

aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650

gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700

tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750

cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800

gatggaaaag atgtatttaa taccaaatct gttgggcttt ctattaaaga 850

ggcaatgact tatcacccca accaggtagt agaaggctgt tgttcagata 900

tggctgttac ttttaatgga ctgactccaa atcagatgca tgtgatgatg 950

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gtaactacat atccaataca gctgtatgtt tctttttctt ttctaatttg 1150

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aagtgtttta agaataataa ttttgcaaat aaactattaa taaatattat 1300

atgtgataaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350

tttgctgatt ggttaaaaaa ttttaacagg tctttagcgt tctaagatat 1400

gcaaatgata tctctagttg tgaatttgtg attaaagtaa aacttttagc 1450

tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctccccaa 1500

gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550

attaaagtga aagttgaaaa at 1572

<210> 341
<211> 318
<212> PRT
<213> Homo Sapien

<400> 341

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Ser Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile
            20                  25                  30

Gly His Gly Asn Arg Met His His His Glu His His His Leu Gln
        35                  40                  45

Ala Pro Asn Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg
    50                  55                  60

Met Glu Leu Ser Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val
65                  70                  75

Lys Pro Lys Asp Val Ser Leu Trp Ala Ala Val Lys Glu Thr Trp
            80                  85                  90

Thr Lys His Cys Asp Lys Ala Glu Phe Phe Ser Ser Glu Asn Val
        95                  100                 105

Lys Val Phe Glu Ser Ile Asn Met Asp Thr Asn Asp Met Trp Leu
    110                 115                 120

Met Met Arg Lys Ala Tyr Lys Tyr Ala Phe Asp Lys Tyr Arg Asp
125                 130                 135

Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr Thr Phe Ala Ile
            140                 145                 150

Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp Pro Ser Gln
        155                 160                 165

Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly Asp Leu Glu Tyr
    170                 175                 180

Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu Ser Met Lys
185                 190                 195

Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro Glu Gln
            200                 205                 210

Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val
        215                 220                 225

Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala
    230                 235                 240

Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile
245                 250                 255

Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys
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260 265 270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
275 280 285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly
290 295 300

His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser
305 310 315

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<210> 342
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 342
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<210> 343
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 343
ctggttcttc cttgcacg 18

<210> 344
<211> 28

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 344
gcccaaatgc cctaaggcgg tatacccc 28

<210> 345
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345
gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 346
gggatgcagg tggtgtctca tgggg 25

<210> 347
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 347
ccctcatgta ccggctcc 18

<210> 348
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 348
ggattctaat acgactcact atagggctca gaaaagcgca acagagaa 48

<210> 349
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 349
ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 350
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<210> 351
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 351
ctatgaaatt aaccctcact aaagggacga ggaagatggg cggatggt 48

<210> 352
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 352
ggattctaat acgactcact atagggcacc cacgcgtccg gctgctt 47

<210> 353
<211> 48
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<213> Artificial Sequence

<220>
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<400> 353
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<210> 354
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 354
ggattctaat acgactcact atagggcttg ctgcggtttt tgttcctg 48

<210> 355
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 355
ctatgaaatt aaccctcact aaagggagct gccgatccca ctggtatt 48

<210> 356
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 356
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<210> 357
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 357
ctatgaaatt aaccctcact aaagggagcc cgggcatggt ctcagtta 48

<210> 358
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 358
ggattctaat acgactcact atagggcggg aagatggcga ggaggag 47

<210> 359
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 359
ctatgaaatt aaccctcact aaagggacca aggccacaaa cggaaatc 48

<210> 360
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 360
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<210> 361
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 361
ctatgaaatt aaccctcact aaagggaggg tacaattaag gggtggat 48

<210> 362
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 362
ggattctaat acgactcact atagggcccg cctcgctcct gctcctg 47

<210> 363
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 363
ctatgaaatt aaccctcact aaagggagga ttgccgcgac cctcacag 48

<210> 364
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
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<400> 364

ggattctaat acgactcact atagggcccc tcctgccttc cctgtcc 47

<210> 365
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<400> 365
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<210> 366
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<400> 366
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<210> 367
<211> 47

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 367
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<210> 368
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 368
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<210> 369
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 369
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<210> 370
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<400> 370
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<210> 371
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<400> 371
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<210> 372
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 372
ggattctaat acgactcact atagggccag ggaaatccgg atgtctc 47

<210> 373
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 373
ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 374
ggattctaat acgactcact atagggccag ctacccgcag gaggagg 47

<210> 375
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 375
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<210> 376
<211> 997
<212> DNA
<213> Homo Sapien

<400> 376
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agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100

aaaaaatgaa ttcatctaaa tcatctgaaa cacaatgcac agagagagga 150

tgcttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200

atttctcagt gcctgtttca tcaccagatg tgttgtgaca tttcgcatct 250

ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300

ctctcctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350

gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400

tttcctgggc gttaagttta aagaactgct cagccatggg ggctcacctg 450

gtggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500

taaaatgaga gagtttttta ttggactgtc agaccaggtt gtcgagggtc 550

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tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900

taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 997

<210> 377
<211> 219
<212> PRT
<213> Homo Sapien

<400> 377

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Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro			
				20					25						30		
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr			
				35					40						45		
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro			
				50					55						60		
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser			
				65					70						75		
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser			
				80					85						90		
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu			
				95					100						105		
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser			
				110					115						120		
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg			
				125					130						135		
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp			
				140					145						150		
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp			
				155					160						165		
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala			
				170					175						180		

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
200 205 210

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<210> 422
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tcaaatccag caatcgaacc ccagtggtac aggaatttga aagtgtggaa 200

ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250

gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300

ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350

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Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu	
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Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr	
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Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr	
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Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly	
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Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val	
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Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg	
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Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val	
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Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val	
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Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly	
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His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu	
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Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe	
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His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
200 205 210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
230 235 240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
245 250 255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
275 280 285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly
290 295 300

Asp Phe Arg His Lys Ser Ser Phe Val Ile
305 310